

570 ID NO: 2

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OM protein - protein search, using sw model	
Run on:	October 29, 2002, 13:59:28 ; Search time 40 Seconds (without alignments) 8.890 Million cell updates/sec
Title:	US-09-674-913a-2
Perfect score:	140
Sequence:	1 RLEAKHRENVPGHERMGRGRTSSKELA 27
Scoring table:	BLOSUM62
Gappen:	10.0 , Gapext 0.5
Searched:	87354 seqs, 13170612 residues
Total number of hits satisfying chosen parameters:	87354
Minimum DB seq length:	0
Maximum DB seq length:	200000000
Post-processing:	Maximum Match 0%
Listing first 45 summaries	
Database :	Published Applications_AA:*
1:	/cgn2_6/ptodata/1/puppa/US08_PUBCOMB.pep:*
2:	/cgn2_6/ptodata/1/puppa/PCT_NEW_PUB.pep:*
3:	/cgn2_6/ptodata/1/puppa/US06_NEW_PUB.pep:*
4:	/cgn2_6/ptodata/1/puppa/US05_PUBCOMB.pep:*
5:	/cgn2_6/ptodata/1/puppa/US07_NEW_PUB.pep:*
6:	/cgn2_6/ptodata/1/puppa/US07_PUBCOMB.pep:*
7:	/cgn2_6/ptodata/1/puppa/US08_NEW_PUB.pep:*
8:	/cgn2_6/ptodata/1/puppa/PCTUS_PUBCOMB.pep:*
9:	/cgn2_6/ptodata/1/puppa/US09_NEW_PUB.pep:*
10:	/cgn2_6/ptodata/1/puppa/US10_NEW_PUB.pep:*
11:	/cgn2_6/ptodata/1/puppa/US10_PUBCOMB.pep:*
12:	/cgn2_6/ptodata/1/puppa/US60_NEW_PUB.pep:*
13:	/cgn2_6/ptodata/1/puppa/US60_PUBCOMB.pep:*
14:	/cgn2_6/ptodata/1/puppa/US60_PUBCOMB.pep:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	
SUMMARIES	
Result No.	Score
1	4.8
2	43.5
3	43
4	43
5	43
6	42
7	42
8	42
9	42
10	42
11	42
12	42
13	42
14	42
15	42
16	42
17	42
18	42
19	42
Query Match Length DB ID	Description
34.3	31 10 US-09-674-761-32237 Sequence 39337, A
31.1	206 10 US-09-815-242-11988 Sequence 11988, A
30.7	88 10 US-09-925-300-1493 Sequence 1493, A
30.7	102 10 US-09-866-761-35901 Sequence 35901, A
30.7	165 10 US-09-811-284-208 Sequence 208, App
44	10 US-09-864-671-34158 Sequence 34158, A
30.0	285 10 US-09-815-242-11860 Sequence 11860, A
30.0	327 10 US-09-815-242-5083 Sequence 5083, App
30.0	560 10 US-09-864-671-31938 Sequence 31938, A
30.0	572 10 US-09-864-761-34546 Sequence 34546, A
30.0	583 10 US-09-810-264-38 Sequence 38, App
30.0	695 10 US-09-794-927-10 Sequence 10, App
30.0	695 10 US-09-794-927-12 Sequence 12, App
30.0	695 10 US-09-794-927-14 Sequence 14, App
30.0	695 10 US-09-795-847-10 Sequence 10, App
30.0	695 10 US-09-795-847-12 Sequence 12, App
30.0	695 10 US-09-795-847-14 Sequence 14, App
30.0	695 10 US-09-794-743-10 Sequence 10, App
30.0	695 10 US-09-794-743-12 Sequence 12, App
20	42 30.0 US-09-794-743-14 Sequence 14, App
21	42 30.0 US-09-794-748-10 Sequence 10, App
22	42 30.0 US-09-794-748-12 Sequence 12, App
23	42 30.0 US-09-794-748-14 Sequence 14, App
24	42 30.0 US-09-794-748-16 Sequence 10, App
25	42 30.0 US-09-794-925-12 Sequence 12, App
26	42 30.0 US-09-794-925-14 Sequence 14, App
27	42 30.0 US-09-681-442-10 Sequence 10, App
28	42 30.0 US-09-681-442-12 Sequence 12, App
29	42 30.0 US-09-681-442-14 Sequence 14, App
30	42 30.0 US-09-681-442-16 Sequence 20, App
31	42 30.0 US-09-794-927-16 Sequence 16, App
32	42 30.0 US-09-794-927-18 Sequence 20, App
33	42 30.0 US-09-794-927-20 Sequence 20, App
34	42 30.0 US-09-795-847-16 Sequence 16, App
35	42 30.0 US-09-795-847-18 Sequence 18, App
36	42 30.0 US-09-795-847-20 Sequence 20, App
37	42 30.0 US-09-794-43-16 Sequence 16, App
38	42 30.0 US-09-794-43-18 Sequence 20, App
39	42 30.0 US-09-794-743-20 Sequence 16, App
40	42 30.0 US-09-794-448-16 Sequence 20, App
41	42 30.0 US-09-794-748-18 Sequence 16, App
42	42 30.0 US-09-794-748-20 Sequence 20, App
43	42 30.0 US-09-794-925-16 Sequence 16, App
44	42 30.0 US-09-794-925-18 Sequence 18, App
45	42 30.0 US-09-794-925-20 Sequence 20, App
ALIGNMENTS	
RESULT 1	US-09-864-761-39237
;	Sequence 39237, Application US/09864761
;	Patent No. US2002048763A1
;	GENERAL INFORMATION:
;	APPLICANT: Penn, Sharron G.
;	APPLICANT: Rank, David R.
;	APPLICANT: Hanzel, David K.
;	APPLICANT: Chen, Weisheng.
;	TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR FILE REFERENCE: Aemotica-X-1.
;	CURRENT APPLICATION NUMBER: US/09/864,761
;	CURRENT FILING DATE: 2001-05-23
;	PRIOR APPLICATION NUMBER: US 60/180,312
;	PRIOR FILING DATE: 2000-02-04
;	PRIOR APPLICATION NUMBER: US 60/207,456
;	PRIOR FILING DATE: 2000-03-26
;	PRIOR APPLICATION NUMBER: US 09/632,366
;	PRIOR FILING DATE: 2000-08-03
;	PRIOR APPLICATION NUMBER: GB 24263,6
;	PRIOR APPLICATION NUMBER: US 60/235,359
;	PRIOR FILING DATE: 2000-09-27
;	PRIOR APPLICATION NUMBER: PCT/US01/00666
;	PRIOR FILING DATE: 2001-01-30
;	PRIOR APPLICATION NUMBER: PCT/US01/00667
;	PRIOR FILING DATE: 2001-01-30
;	PRIOR APPLICATION NUMBER: PCT/US01/00668
;	PRIOR FILING DATE: 2001-01-30
;	PRIOR APPLICATION NUMBER: PCT/US01/00669
;	PRIOR FILING DATE: 2001-01-30
;	PRIOR APPLICATION NUMBER: PCT/US01/00665
;	PRIOR FILING DATE: 2001-01-30
;	PRIOR APPLICATION NUMBER: PCT/US01/00661
;	PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 60/234,687
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 2000-05-30
 PRIOR APPLICATION NUMBER: US 09/774,203
 NUMBER OF SEQ ID NOS: 49117
 SOFTWARE: Amomax Sequence Listing Engine vers. 1.1
 SEQ ID NO 39237
 LENGTH: 31
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AC006538.1
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.3
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.3
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.3
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.1
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4
 US-09-864-761-39237

RESULT 2
 Query Match 34.3%; Score 48; DB 10; Length 31;
 Best Local Similarity 50.0%; Pred. No. 0.69; 8; Indels 0; Gaps 0;
 Matches 10; Conservative 2; Mismatches 8; SEQ ID NO 1493
 DB 4 EPVPGHARPGHQSRGSEAA 23

US-09-815-242-11988
 Sequence 11988 Application US/09815242
 Patent No. US20020061569A1
 GENERAL INFORMATION:
 - APPLICANT: Baselbeck, Robert
 - APPLICANT: Ohlsen, Kari L.
 - APPLICANT: Zyskind, Judith W.
 - APPLICANT: Wall, Daniel
 - APPLICANT: Trawick, John D.
 - APPLICANT: Carr, Grant J.
 - APPLICANT: Yamamoto, Robert T.
 - APPLICANT: Xu, H. Howard
 TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes
 FILE REFERENCE: ELITRA.01A
 CURRENT APPLICATION NUMBER: US/09/815,242
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 NUMBER OF SEQ ID NOS: 1410
 SOFTWARE: FASTSEQ for Windows Version 4.0
 LENGTH: 206
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa

RESULT 3
 US-09-925-300-1493
 Sequence 1493 Application US/09925300
 Patent No. US20020151681A1
 GENERAL INFORMATION:
 - APPLICANT: Craig Rosen,
 - APPLICANT: Steve Rubin,
 - APPLICANT: Nucleic Acids, Proteins and Antibodies
 TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 FILE REFERENCE: PA101
 CURRENT APPLICATION NUMBER: US/09/925,300
 CURRENT FILING DATE: 2001-08-10
 PRIOR APPLICATION NUMBER: PCT/US00/05988
 PRIOR FILING DATE: 2000-03-08
 PRIOR APPLICATION NUMBER: 60/124,270
 PRIOR FILING DATE: 1999-03-12
 NUMBER OF SEQ ID NOS: 1890
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 1493
 LENGTH: 88
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (10)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 NAME/KEY: SITE
 LOCATION: (29)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 NAME/KEY: SITE
 LOCATION: (73)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-09-925-300-1493

RESULT 4
 Query Match 30.7%; Score 43; DB 10; Length 88;
 Best Local Similarity 47.1%; Pred. No. 11; 3; Mismatches 8; Indels 6; Gaps 0;
 Matches 8; Conservative 3; Mismatches 8; SEQ ID NO 1493
 DB 46 TEKSWRELVPGHKEMSQ 62

US-09-864-761-35901
 Sequence 35901 Application US/09864761
 Patent No. US2002048763A1
 GENERAL INFORMATION:
 - APPLICANT: Penn, Sharron G.
 - APPLICANT: Rank, David R.
 - APPLICANT: Hanzel, David K.
 - APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENE EXPRESSION ANALYSIS BY MICROARRAY
 FILE REFERENCE: Aeonica-X-1
 CURRENT APPLICATION NUMBER: US/09/864,761
 CURRENT FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263.6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00670
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00672
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00674
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 60/234,687
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/774,203
 PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 4917
 SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
 SEQ ID NO: 35901
 LENGTH: 102
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AL096678.8
 OTHER INFORMATION: EXPRESSED IN BP474, SIGNAL = 1.1
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.96
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.98
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.1
 OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.9
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
 OTHER INFORMATION: EST_HUMAN HIT: BE792924.1, EVALUATE 1.40e-01
 S-09-864-761-35901

Query Match 30.7%; Score 43; DB 10; Length 102;
 Best Local Similarity 37.5%; Pred. No. 13; Matches 9; Conservative 3; Mismatches 12; Indels 0; Gaps 0; Length: 102

QY 2 LEAKRENPGHGRMGRGRTSSKE 25
 4 LEIKEKPEAGHAEERGETEDQ 27

RESULT 5
 US 09-811-284-208
 Sequence 208, Application US/09811284
 ; Patent No. US20020058306A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Vogeli, Gabriel
 ; TITLE OF INVENTION: No. US20020058306A1 G Protein-Coupled Receptors
 ; FILE REFERENCE: 00167US1
 ; CURRENT APPLICATION NUMBER: US/09/811,284
 ; CURRENT FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/189,783
 ; PRIOR FILING DATE: 2000-03-16
 ; PRIOR APPLICATION NUMBER: 60/189,907
 ; PRIOR FILING DATE: 2000-03-16
 ; PRIOR APPLICATION NUMBER: 60/189,918
 ; PRIOR FILING DATE: 2000-03-16
 ; PRIOR APPLICATION NUMBER: 60/189,960
 ; PRIOR FILING DATE: 2000-03-16
 ; PRIOR APPLICATION NUMBER: 60/189,917
 ; PRIOR FILING DATE: 2000-03-16
 ; PRIOR APPLICATION NUMBER: 60/192,945
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: 60/192,830
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: 60/192,935
 ; PRIOR FILING DATE: 2000-03-29
 ; NUMBER OF SEQ ID NOS: 258
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 208
 ; LENGTH: 165
 ; TYPE: PPT
 ; ORGANISM: Homo sapiens
 ; US-09-811-284-208

Query Match 30.7%; Score 43; DB 10; Length 165;
 Best Local Similarity 42.1%; Pred. No. 21; Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0; Length: 165

QY 5 KIRENVPGHGRMGRGRTSS 23
 Db 46 KRESLPSQNRRSSGTSVS 64

RESULT 6
 US-09-864-761-34158
 ; Sequence 34158, Application US/09864761
 ; Patent No. US20020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
 ; FILE REFERENCE: Aeonica-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00564
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00655
 ; PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00663
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00662
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00661
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 60/234,687
 PRIOR FILING DATE: 2000-09-21
 SEQ ID NO: 34158
 LENGTH: 44
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO APP000089.1
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.6
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.1
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.5
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3
 OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 4.1
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.4
 OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.5
 OTHER INFORMATION: EST-HUMAN HIT: AUI31304.1, EVALUE 2.00e-19
 OTHER INFORMATION: SWISSPROT HIT: Q95241, EVALUE 2.00e-20
 US-09-864-761-34158

Query Match 30.0%; Score 42; DB 10; Length 44;
 Best Local Similarity 80.0%; Pred. No. 7.2; Matches 1; Mismatches 1; Indels 0; Gaps 0; Gaps 0;

Qy 1 RLEAKHREN 10
 ||||||| :
 Db 33 RLEAKHREM 42

RESULT 7

US-09-815-242-11860
 Sequence 11860, Application US/09815242
 Patent No. US2002020061569A1
 GENERAL INFORMATION:
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Kari L.
 APPLICANT: Zyskind, Judith W.
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John D.
 APPLICANT: Carr, Grant J.
 APPLICANT: Yamamoto, Robert T.
 APPLICANT: Xu, H. Howard
 TITLE OF INVENTION: Identification of Essential Genes in
 FILE REFERENCE: ELITRA.011A
 CURRENT APPLICATION NUMBER: US/09/815,242
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2001-03-23
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 5083
 LENGTH: 327
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa

RESULT 8

US-09-815-242-5083
 Sequence 5083, Application US/09815242
 Patent No. US20020061569A1
 GENERAL INFORMATION:
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Kari L.
 APPLICANT: Zyskind, Judith W.
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John D.
 APPLICANT: Carr, Grant J.
 APPLICANT: Yamamoto, Robert T.
 APPLICANT: Xu, H. Howard
 TITLE OF INVENTION: Identification of Essential Genes in
 FILE REFERENCE: ELITRA.011A
 CURRENT APPLICATION NUMBER: US/09/815,242
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2001-03-23
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 5083
 LENGTH: 327
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa

RESULT 9

US-09-815-242-5083
 Query Match 30.0%; Score 42; DB 10; Length 327;
 Best Local Similarity 44.4%; Pred. No. 61; Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0; Gaps 0;

Qy 1 RLEAKHRENPGHERMGR 18
 | : ||| : | | :
 Db 48 RADPRHREALGEMRLWR 65

US-09-864-761-37938
 Sequence 37938, Application US/09864761
 ; Patent No. US20020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 FILE REFERENCE: Acomica-X-1
 CURRENT APPLICATION NUMBER: US/09/864,751
 CURRENT FILING DATE: 2001-05-23
 CURRENT APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: GB 24263,6
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: US/09/632,366
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: GB 24263,6
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
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 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00670
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 60/234,687
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 60/608,408
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/774,203
 PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 49117
 SOFTWARE: Annotrax Sequence Listing Engine vers. 1.1
 SEQ ID NO 37938
 LENGTH: 560
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AC005074.1
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.5
 OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.8
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.93
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.99
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
 OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.8
 OTHER INFORMATION: EST HUMAN HIT: AW916211.1, EVALUE 2.00e-91
 OTHER INFORMATION: SWISSPROT HIT: P53935, EVALUE 2.00e-03
 US-09-864-761-37938
 Query Match 30.0%; Score 42; DB 10; Length 560;
 Best Local Similarity 41.7%; Pred. No. 1.1e+02;
 Matches 10; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

US-09-864-761-34546
 Sequence 34546, Application US/09864761
 ; Patent No. US20020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 FILE REFERENCE: Acomica-X-1
 CURRENT APPLICATION NUMBER: US/09/864,761
 CURRENT FILING DATE: 2001-05-23
 CURRENT APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: US/09/632,366
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: GB 24263,6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00663
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00662
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/774,203
 PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 49117
 SOFTWARE: Annotrax Sequence Listing Engine vers. 1.1
 SEQ ID NO 34546
 LENGTH: 572
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AC005089.2
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3
 OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 5.4
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4
 OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 5.6
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.3
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.1
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.7
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.1

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; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.7
; OTHER INFORMATION: SWISSPROT HIT: P39357, EVALUE 2.00e-03
; OTHER INFORMATION: EST_HUMAN HIT: AW96211.1, EVALUE 2.00e-91
US-09-864-761-34546

Query Match 30.0%; Score 42; DB 10; Length 572;
Best Local Similarity 41.7%; Pred. No. 1.1e+02; 7; Indels 2; Gaps 1;
Matches 10; Conservative 5; Mismatches 7; DB 525

RESULT 11
US-09-810-264-38
; Sequence 38, Application US/09810264
; Patent No. US20020076775A1
; GENERAL INFORMATION:
; APPLICANT: Crane, Virginia C.
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Hu, Xu
; APPLICANT: Lu, Guihua
; APPLICANT: Zhang, Linyu
; TITLE OF INVENTION: WRKY Transcription Factors and Methods
; TITLE OF INVENTION: of Use
; FILE REFERENCE: 1183
; CURRENT APPLICATION NUMBER: US/09/810, 264
; CURRENT FILING DATE: 2001-03-16
; PRIORITY APPLICATION NUMBER: US 60/190,467
; PRIORITY FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 38
; LENGTH: 583
; TYPE: PRT
; ORGANISM: Zea mays
US-09-810-264-38

RESULT 12
US-09-794-927-10
; Sequence 10, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Blenkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 12834176280FG
; CURRENT APPLICATION NUMBER: US/09/794, 927
; CURRENT FILING DATE: 2001-02-27
; PRIORITY APPLICATION NUMBER: 09/416, 901
; PRIORITY FILING DATE: 1999-10-13
; PRIORITY APPLICATION NUMBER: 60/155, 493
; PRIORITY FILING DATE: 1999-09-23
; PRIORITY APPLICATION NUMBER: 09/404, 133
; PRIORITY FILING DATE: 1999-09-23
; PRIORITY APPLICATION NUMBER: PCT/US99/20881
; PRIORITY FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 12
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-927-12

RESULT 13
US-09-794-927-12
; Sequence 12, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Blenkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 12834176280FG
; CURRENT APPLICATION NUMBER: US/09/794, 927
; CURRENT FILING DATE: 2001-02-27
; PRIORITY APPLICATION NUMBER: 09/416, 901
; PRIORITY FILING DATE: 1999-10-13
; PRIORITY APPLICATION NUMBER: 60/155, 493
; PRIORITY FILING DATE: 1999-09-23
; PRIORITY APPLICATION NUMBER: 09/404, 133
; PRIORITY FILING DATE: 1999-09-23
; PRIORITY APPLICATION NUMBER: PCT/US99/20881
; PRIORITY FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 12
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-927-14

RESULT 14
US-09-794-927-14
; Sequence 14, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Blenkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES

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TITLE OF INVENTION: THEREFOR
 FILE REFERENCE: 28341/6280FG
 CURRENT APPLICATION NUMBER: US/09/794,927
 CURRENT FILING DATE: 2001-02-27

PRIOR APPLICATION NUMBER: 09/416,901
 PRIOR FILING DATE: 1999-10-13
 PRIOR APPLICATION NUMBER: 60/155,493
 PRIOR FILING DATE: 1999-09-23

PRIOR APPLICATION NUMBER: 09/404,133
 PRIOR FILING DATE: 1999-09-23
 PRIOR APPLICATION NUMBER: PCT/US99/20881

PRIOR FILING DATE: 1999-09-23
 PRIOR APPLICATION NUMBER: 60/101,594
 PRIOR FILING DATE: 1998-09-24

NUMBER OF SEQ ID NOS: 73
 SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 14
 LENGTH: 695
 TYPE: PRT

ORGANISM: Homo sapiens

AS-09-794-927-14
 Query Match Similarity 30.0%; Score 42; DB 10; Length 695;
 Best Local Similarity 80.0%; Pred. No. 1.4e+02; 1; Mismatches 0;
 Matches 8; Conservative 1; Indels 0; Gaps 0;

Qy 1 RLEAKHENV 10
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 Db 322 RLEAKHREM 331

RESULT 15

US-09-795-847-10
 Sequence 10, Application US/09795847

Patent No. US20010018208A1

GENERAL INFORMATION:

APPLICANT: Gurney, Mark E.

APPLICANT: Bielkowski, Michael J.

APPLICANT: Heinrikson, Robert L.

APPLICANT: Parodi, Luis A.

APPLICANT: Yan, Riqiang

TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES

TITLE OF INVENTION: THEREFOR

FILE REFERENCE: 28341/6280DE

CURRENT APPLICATION NUMBER: US/09/795,847

PRIOR APPLICATION NUMBER: 09/416,901

CURRENT FILING DATE: 2001-02-28

PRIOR APPLICATION NUMBER: 60/155,493

PRIOR FILING DATE: 1999-10-13

PRIOR APPLICATION NUMBER: 60/155,493

PRIOR FILING DATE: 1999-09-23

PRIOR APPLICATION NUMBER: 09/404,133

PRIOR FILING DATE: 1999-09-23

PRIOR APPLICATION NUMBER: PCT/US99/20881

PRIOR FILING DATE: 1999-09-23

PRIOR APPLICATION NUMBER: 60/101,594

PRIOR FILING DATE: 1998-09-24

NUMBER OF SEQ ID NOS: 73

SOFTWARE: PatentIn Ver. 2.0

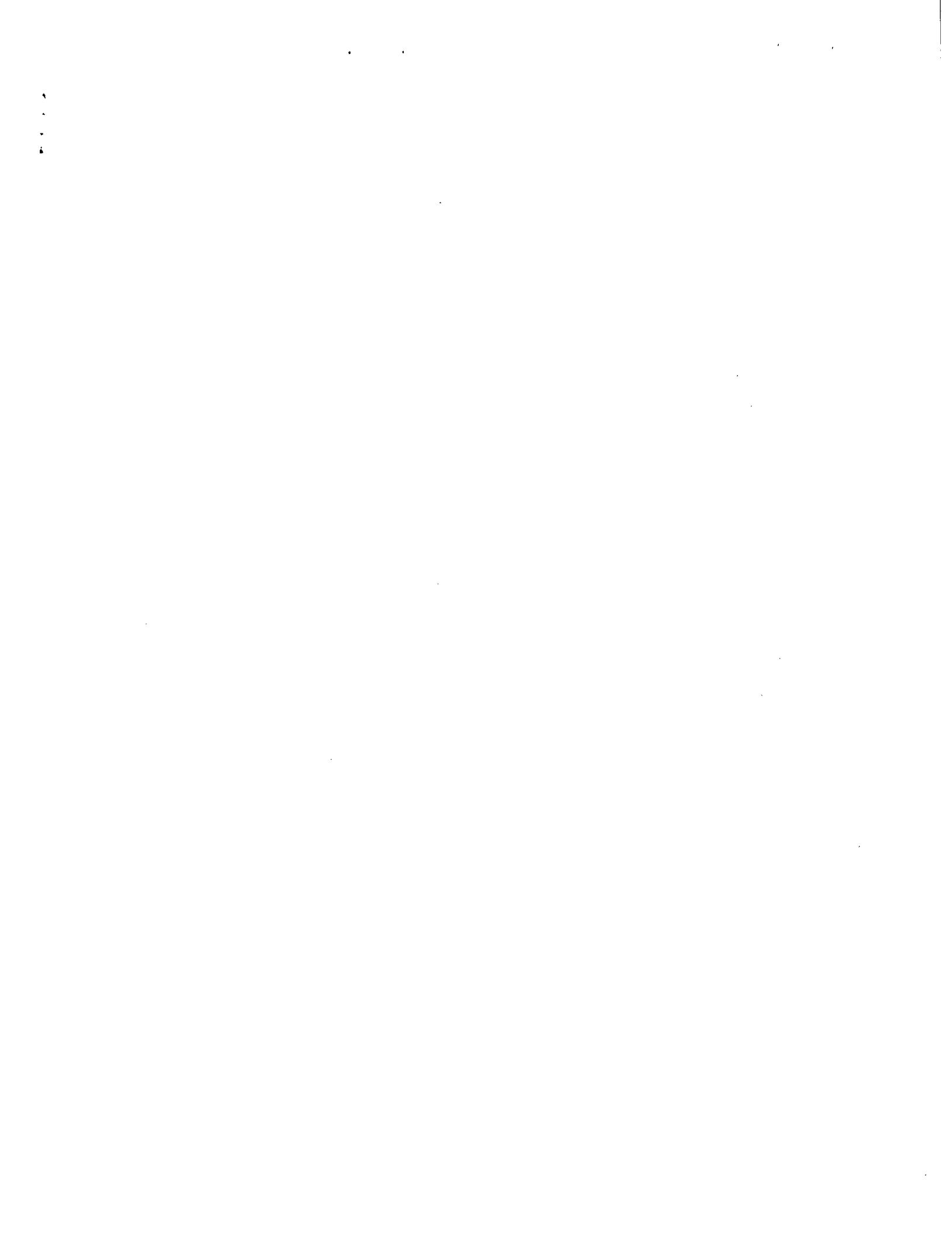
SEQ ID NO: 10
 LENGTH: 695
 TYPE: PRT

ORGANISM: Homo sapiens

Search completed: October 29, 2002, 14:07:51
 Job time : 40 secs

Query Match Similarity 30.0%; Score 42; DB 10; Length 695;
 Best Local Similarity 80.0%; Pred. No. 1.4e+02; 1; Mismatches 0;
 Matches 8; Conservative 1; Indels 0; Gaps 0;

Qy 1 RLEAKHENV 10
 |||||||:
 Db 322 RLEAKHREM 331



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OM protein - protein search, using sw model

Run on: October 29, 2002, 13:57:43 ; Search time 26 Seconds

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Scoring table: BLOSUM62 30.555 Million cell updates/sec

Title: US-09-674-913A-2

Perfect score: 140

Sequence: 1 RLEAKHRENVPGHERMGRGRTSSKELA 27

Scoring table: Gapext 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description	
1	109	77.9	25	2	US-08-726-306A-61	Sequence 61, Appl	
2	109	77.9	25	2	US-08-726-306A-87	Sequence 87, Appl	
3	50	35.7	26	1	US-07-942-245-321	Sequence 321, Appl	
4	47	33.6	10	2	US-08-726-306A-1	Sequence 1, Appl	
5	46	32.9	26	1	US-07-942-245-312	Sequence 312, Appl	
45	5.5	32.5	537	4	US-09-134-001C-4091	Sequence 4091, Appl	
6	7	44	31.4	26	1	US-07-942-245-314	Sequence 314, Appl
8	8	44	31.4	26	1	US-07-942-245-315	Sequence 315, Appl
9	9	44	31.4	26	1	US-07-942-245-349	Sequence 349, Appl
10	10	44	31.4	295	4	US-09-026-482B-2	Sequence 2, Appl
11	11	44	31.4	617	4	US-09-134-001C-4012	Sequence 4012, Appl
12	12	43	30.7	25	1	US-07-942-245-311	Sequence 311, Appl
13	13	43	30.7	119	1	US-08-584-528A-1	Sequence 1, Appl
14	14	30.7	119	5	PCT-US94-07793-7	Sequence 7, Appl	
15	15	43	30.7	161	2	US-08-581-528A-6	Sequence 6, Appl
16	16	43	30.7	161	5	PCT-US94-07793-6	Sequence 5, Appl
17	17	43	30.7	855	2	US-08-816-693A-2	Sequence 2, Appl
18	18	43	30.7	855	3	US-08-815-291-2	Sequence 3, Appl
19	19	43	30.7	855	4	US-09-496-672-2	Sequence 2, Appl
20	20	42	30.0	17	5	PCT-US92-09070-8	Sequence 5, Appl
21	21	42	30.0	25	1	US-07-942-245-302	Sequence 1, Appl
22	22	42	30.0	30	2	US-08-726-306A-59	Sequence 2, Appl
23	23	42	30.0	38	1	US-08-255-155A-45	Sequence 1, Appl
24	24	42	30.0	40	5	PCT-US92-09070-5	Sequence 5, Appl
25	25	42	30.0	50	4	US-08-314-268-159	Sequence 4, Appl
26	26	42	30.0	68	1	US-07-755-250-10	Sequence 1, Appl
27	27	42	30.0	129	1	US-08-360-914B-15	Sequence 15, Appl

ALIGNMENTS

US-08-726-306A-61

RESULT 1

US-08-726-306A-61

Sequence 61, Application US/08726306A

Patent No. 5958684

GENERAL INFORMATION:

APPLICANT: van Leeuwen, Frederik Willem

APPLICANT: Bubbach, Johannes Peter Heinrich

APPLICANT: Giesveld, Franklin G.

TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS

NUMBER OF SEQUENCES: 189

CORRESPONDENCE ADDRESS:

ADRESSEE: Banner & Witcoff, Ltd.

STREET: 1 Financial Center

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02111

COMPUTER READABLE FORM:

COMPUTER TYPE: Diskette, 3.50 inch, 1.44 MB storage

OPERATING SYSTEM: PC-MS-DOS

SOFTWARE: Wordperfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/726,306A

FILED DATE: 02-Oct-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 95/20080.4

FILED DATE: 02-Oct-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/009,832

APPLICATION NUMBER: US 60/009,832

FILED DATE: 01-Oct-1996

ATTORNEY/AGENT INFORMATION:

NAME: Williams, Ph.D., Kathleen M.

REGISTRATION NUMBER: 34,380

REFERENCE/DOCKET NUMBER: 95,048-A (3255/00784)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 345-9111

TELEFAX: (617) 345-9111

INFORMATION FOR SEQ ID NO: 61:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: protein

Query Match Best Local Similarity 77.9%; Score 109; DB 2; Length 25; Matches 21; Conservative 100.0%; Pred. No. 1.3e-11; Mismatches 0; Indels 0; Gaps 0;

REFERENCE/DOCKET NUMBER: 96-048-A (3255/00784)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 345-9100

TELEFAX: (617) 345-9111

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-126-3066A-1

Query Match

Score 47; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.084; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 RGRTSSKELA 27

1 RGRTSSKELA 10

RESULT 5
Sequence 312, Application US/07942245
Patent No. 5639641

GENERAL INFORMATION:

APPLICANT: PEDERSEN, Jan T.

APPLICANT: SEARLE, Stephen M.J.

APPLICANT: REES, Anthony R.

APPLICANT: ROGUSKA, Michael A.

APPLICANT: GUILDFORD, Brydon C.

TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT

NUMBER OF SEQUENCES: 522

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas

STREET: 2100 Pennsylvania Avenue, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: United States

ZIP: 20037-3202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: UNIX

SOFTWARE: In house

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/942,245

FILING DATE: 09-SEP-1992

CLASSIFICATION: 530

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 293-7060

TELEFAX: (202) 293-7860

TELEX: 6491103

INFORMATION FOR SEQ ID NO: 312:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-07-942-245-312

Query Match 32.9%; Score 46; DB 1; Length 26;

Best Local Similarity 45.0%; Pred. No. 0.4; Mismatches 9; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Matches 9; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 3 EAKHRENPGHGRGRGRMS 22

Db 5 ELKPGKGTGPGHEKKGTSSMS 24

US-09-134-001C-4091

Sequence 4091, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GIC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIORITY APPLICATION NUMBER: US 60/064,964

PRIORITY FILING DATE: 1997-11-08

PRIORITY FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 4091

LENGTH: 537

TYPE: PRT

ORGANISM: Staphylococcus epidermidis

US-09-134-001C-4091

Query Match 32.5%; Score 45.5; DB 4; Length 537;

Best Local Similarity 55.0%; Pred. No. 21; Mismatches 3; Indels 5; Gaps 1;

Matches 11; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 9 NVPGH-ERMGGRGRSSKELA 27

Db 186 NLPGHVEAMGSVQTSPLTLA 205

RESULT 7
Sequence 314, Application US/07942245

Patent No. 5639641

GENERAL INFORMATION:

APPLICANT: PEDERSEN, Jan T.

APPLICANT: SEARLE, Stephen M.J.

APPLICANT: REES, Anthony R.

APPLICANT: ROGUSKA, Michael A.

TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT

NUMBER OF SEQUENCES: 522

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas

STREET: 2100 Pennsylvania Avenue, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: United States

ZIP: 20037-3202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: HP 9000/700 Workstation

OPERATING SYSTEM: UNIX

SOFTWARE: In house

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/942,245

FILING DATE: 09-SEP-1992

CLASSIFICATION: 530

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 293-7060

TELEFAX: 6491103

INFORMATION FOR SEQ ID NO: 314:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-07-942-245-314

Query Match 31.4%; Score 44; DB 1; Length 26;

Best Local Similarity 40.0%; Pred. No. 0.86; Length 26;

RESULT 6

Matches 8; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

RESULT 8
US-07-942-245-315
; Sequence 315, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: HP 9000/700 Workstation
; OPERATING SYSTEM: UNIX
; SOFTWARE: In house
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/942,245
; FILING DATE: 09-SEP-1992
; CLASSIFICATION: 530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 315:
; - SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-942-245-315

Query Match 31.4%; Score 44; DB 1; Length 26;
Best Local Similarity 45.0%; Pred. No. 0.86; Matches 9; Indels 0; Gaps 0;

Matches 9; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 EAKHRENVPGHERMGRRTS 22
Db 5 ELKPGKGTGHEKGTSSTS 24

RESULT 9
US-07-942-245-349
; Sequence 349, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.

Query Match 31.4%; Score 44; DB 1; Length 26;
Best Local Similarity 45.0%; Pred. No. 0.86; Matches 9; Indels 0; Gaps 0;

Matches 9; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 EAKHRENVPGHERMGRRTS 22
Db 5 ELKPGKGTGHEKGTSSTS 24

RESULT 10
US-09-026-482B-2
; Sequence 2, Application US/09026482B
; Patent No. 613538
; GENERAL INFORMATION:
; APPLICANT: REISER, STEVEN E.
; APPLICANT: SOMMERVILLE, CHRIS
; TITLE OF INVENTION: ACYL-COA REDUCTASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PAUL A. GOTTLIEB, AGCTT
; ADDRESSEE: DEPARTMENT OF ENERGY
; ADDRESS: IGC-62 (FORSTI) MS-6F 067
; STREET: 1000 INDEPENDENCE AVE. S.W.
; CITY: WASHINGTON, D.C.
; ZIP: 20585
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORDPERFECT 6.22
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,482B
; ATTORNEY/AGENT INFORMATION:
; NAME: ALMAN, JOY
; REGISTRATION NUMBER: 40486
; FILING DATE: 02/19/98
; REFERENCE/DOCKET NUMBER: S-87814
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 630-252-2179
; TELEFAX: 630-252-2779
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 295 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-026-482B-2

Query Match 31.4%; score 44; DB 4; Length 295;
 Best Local Similarity 39.4%; Pred. No. 18;
 Matches 13; Conservative 4; Mismatches 1;
 TYPE: amino acid
 TOPOLogy: linear
 MOLECULE TYPE: peptide
 US-07-942-245-311

Query Match 30.7%; Score 43; DB 1; Length 26;
 Best Local Similarity 40.0%; Pred. No. 1.3;
 Matches 8; Conservative 3; Mismatches 9;
 Indels 0; Gaps 0;

QY 3 EAKHRENVPGHMRGGRTS 22
 | : : ||| : ||| : |||
 Db 5 ELRPKGKTPGHEKKGTS 24

Query Match 31.4%; Score 44; DB 4; Length 617;
 Best Local Similarity 50.0%; Pred. No. 44;
 Matches 7; Conservative 4; Mismatches 3;
 Indels 0; Gaps 0;

QY 3 EAKHRENVPGHMRGGRTS 22
 | : : ||| : ||| : |||
 Db 92 EDKHEKDVRGHLKL 105

RESULT 12

Sequence 311; Application US/07942245
 Patent No. 5639641
 GENERAL INFORMATION:
 APPLICANT: PEDERSEN, Jan T.
 APPLICANT: SEARLE, Stephen M.J.
 APPLICANT: REES, Michael A.
 APPLICANT: ROUSKA, Braydon C.
 APPLICANT: GUILD, Anthony R.
 APPLICANT: SURFACE RESIDUE VENEERING OF RODENT
 TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
 NUMBER OF SEQUENCES: 522

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
 STREET: 2100 Pennsylvania Avenue, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: United States
 ZIP: 20037-3122

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOSE/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/581,528A
 FILING DATE: 03-Sept-1993
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/089,670
 FILING DATE: 09-JUN-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Lisa A. Haile, Ph.D.
 REGISTRATION NUMBER: 38,347
 REFERENCE DOCKET NUMBER: 07265/081001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619/678-5070
 TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 119 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 IMMEDIATE SOURCE:
 CLONE: GDF-7
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..119

US-08-581-528A-7

Query Match 30.7%; Score 43; DB 2; Length 119;
 Best Local Similarity 50.0%; Pred. No. 8.3;
 Matches 9; Conservative 0; Mismatches 6;
 Indels 0; Gaps 0;

QY 12 GHERMGRGRSSKEI 26

APPLICATION NUMBER: US/07/942,245
 FILING DATE: 09-SEP-1992
 CLASSIFICATION: 530
 COMPUTER: HP 9000/700 Workstation
 OPERATING SYSTEM: UNIX
 SOFTWARE: In house
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/942,245
 FILING DATE: 09-SEP-1992
 CLASSIFICATION: 530
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 293-7060
 TELEFAX: (202) 293-8600

Db 9 GHGRRGRSRCSRKSL 23
 ||| | | | | | | |
 Sequence 7, Application PC/TUS94/07799

RESULT 14
 PCT-US94-07799-7
 GENERAL INFORMATION:
 APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
 TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-7
 NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:
 ADDRESS: Spansley Horn Jubas & Lubitz
 STREET: 1880 Century Park East, Suite 500
 CITY: Los Angeles
 STATE: California
 COUNTRY: USA
 ZIP: 90067

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/07799
 FILING DATE: 08-JUL-1994
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: TUMARKIN LISA A., PH.D.
 REFERENCE NUMBER: P-38,347
 REGISTRATION NUMBER: FD-2348
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 455-5100
 TELEFAX: (619) 455-5110

INFORMATION FOR SEQ ID NO: 7:
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 119 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 IMMEDIATE SOURCE:
 CLONE: GDF-7

FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..119

PCT-US94-07799-7

RESULT 15
 US-08-581-528A-6

; Sequence 6, Application US/08581528A
 ; Patent No. 5,986,058
 ; GENERAL INFORMATION:
 ; APPLICANT: Lee, Se-Jin
 ; APPLICANT: Huyrh, Thanh
 ; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-7
 ; NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:
 ADDRESSE: Fish & Richardson, P.C.
 STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/089,670
 FILING DATE: 09-JUL-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Lisa A. Haile, Ph.D.
 REGISTRATION NUMBER: 38,347
 REFERENCE/DOCKET NUMBER: 07265/081001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619/678-5070
 TELEFAX: 619/678-5099
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 161 amino acids
 TYPE: amino acid
 TOPOLOGY: Linear
 MOLECULE TYPE: protein

US-08-581-528A-6

Query Match 30.7%; Score 43; DB 2; Length 161;
 Best Local Similarity 60.0%; Pred. No. 12; Mismatches 6;
 Matches 9; Conservative 0; Mismatches 6;
 Indels 0; Gaps 0;

QY 12 GHERMGRGRTSSKEL 26
 Db 51 GHGRRGRSRCSRKSL 65

Search completed: October 29, 2002, 14:06:26
 Job time : 27 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on:

October 29, 2002, 13:55:48 ; Search time 31 Seconds

(without alignments) 116.057 Million cell updates/sec

Title: US-09-674-913a-2

Perfect score: 140
Sequence: 1 RLEAKHRENVPGVHERRMGRRTSSKELA 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Minimum DB seq length: 0

Maximum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /SIDS2/gcgatata/geneseq/geneseq/geneseqp-emb1/AA1982.DAT:*

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22: /SIDS2/gcgatata/geneseq/geneseqp-emb1/AA2001.DAT:*

23: /SIDS2/gcgatata/geneseq/geneseqp-emb1/AA2002.DAT:*

ALIGNMENTS

RESULT 1
ID AAY53392
XX AAY53392 standard; peptide; 27 AA.

AC AAY53392;

XX DT 15-FEB-2000 (first entry)

XX DE Mutant beta-APP protein peptide sequence SEQ ID NO:2.

XX KW Mutant; beta-amyloid precursor protein; beta-APP; ubiquitin-B; vaccine;

XX KW Alzheimer's disease; Down syndrome; T cellular immunity; neuroprotective;

XX KW gene therapy.

OS Syntetic.

OS Homo sapiens.

PN W09938564-A1.

XX PD 18-NOV-1999.

XX PF 30-APR-1999; 99W0-N000141.

XX PR 08-MAY-1998; 98NO-0002098.

XX PA (NHYD) NORSK HYDRO AS.

XX PI Gaudernack G, Eriksen JA, Moller M;

XX DR WPI; 2000-039070/03.

XX PT Frameshift mutant beta-amyloid precursor and ubiquitin-B peptides,

XX PT useful for treating Alzheimer's disease and Down syndrome -

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	140	100.0	27 21 AAY56392	Mutant beta-APP pr
2	140	100.0	28 19 AAY121521	Human beta-APP exo
3	140	100.0	22 48 AAB99217	Beta-amyloid precur
4	109	77.9	25 19 AAY20119	Human beta-amyloid
5	109	77.9	300 18 AAY18643	Fragmented human a
6	99	70.7	19 21 AAY56391	Mutant beta-APP pr
7	97	69.3	28 19 AAY21522	Human beta-APP exo
8	93	66.4	17 21 AAY56393	Mutant beta-APP pr
9	82.5	58.9	19 22 AAB99216	AMY peptide. Uni
10	63	45.0	14 22 AAB99215	AMY peptide. Uni

XX
 PS- Claim 10; Page 27; 33pp; English.
 XX
 CC The present invention describes frameshift mutant beta-amyloid precursor
 CC peptides (beta-APP) (AY156301 to AAY53394) and mutant ubiquitin-B
 CC (UBI-B) (AY056395 to AAY56400) associated with Alzheimer's disease and
 CC Down syndrome eliciting T cellular immunity. The peptides may be used as
 CC a vaccine for Alzheimer's disease and Down syndrome. The vaccination is
 CC sufficient to induce specific T-cell immunity to mutant beta-APP and/or
 CC Ubi-B peptides that are associated with Alzheimer's disease or Down
 CC syndrome. The patient may be stimulated in vivo or ex vivo with the
 CC peptides. The peptides and DNA encoding the peptides can also be used for
 CC the treatment or prophylaxis of Alzheimer's disease or the treatment of
 CC Down syndrome.
 XX
 SQ Sequence 27 AA;

Query Match 100.0%; Score 140; DB 21; Length 27;
 Best local similarity 100.0%; Pred. No. 6.9e-16;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

27 1 RLEAKHRENVPGHERMGRGRTSSKELA 27
 Db 1 RLEAKHRENVPGHERMGRGRTSSKELA 27

RESULT 2
 AAY21521
 ID AAY21521 standard; Protein; 28 AA.
 XX
 AC AAY21521;
 XX
 DT 22-JUL-1999 (first entry)
 XX
 DE Human beta-APP exon 9 protein fragment.
 XX
 KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
 KW frameshift mutation; age-related disease; neurodegenerative disorder;
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
 KW ubiquitin B; apolipoprotein B; MAP2; neurofilament-L; neurofilament-M;
 KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
 KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUP-1;
 KW bcl-2; B-cell leukaemia/lymphoma 2 proto-oncogene; HMG-C; NSP-A;
 KW high mobility group protein-C; neuroendocrine specific protein A.
 KW
 Homo sapiens.
 WO9845322-A2.
 XX
 PD 15-OCT-1998.
 XX
 PF 02-APR-1998; 98WO-1B00705.
 XX
 PR 10-APR-1997; 97US-0043163.
 XX
 PA (URUT-) RIJKSUNIV Utrecht.
 PA (ROYA-) ROYAL NETHERLANDS AKADEMIE VAN WETENSCHAPPE.
 PA (UFRD-) UNIV ROTTERDAM ERASMUS.
 XX
 PT Burbach JPH, Grosfeld FG, Van Leeuwen FW;
 XX
 WPI; 1998-609901/51.
 DR N-PSDB; AAX7571.

XX
 PT Diagnosing disease by detecting frameshift mutations in RNA or
 PT corresponding protein mutations - used to diagnose cancer and
 PT neurological diseases, particularly Alzheimer's disease, and also
 PT for treatment and prevention with specific ribozymes or wild-type
 RNA
 XX
 PS Disclosure; Figure 20; 258pp; English.

XX
 CC The present invention relates to a method for detecting a disease or
 pathological condition associated with molecular misreading or coding

XX
 CC This invention describes a novel method for the diagnosis of a disease
 CC caused by, or associated with, an RNA molecule that has a frameshift
 CC mutation. The method is used to diagnose age-related diseases, especially
 CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
 CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
 CC and many others listed) or susceptibility to these disorders. The method
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,
 CC at an early stage. It is based on the observation that disease may be
 CC caused by mutations in RNA rather than DNA. The invention describes the
 CC use of neuronal system RNA molecules, specifically proteins including
 CC beta-amyloid precursor protein (beta-APP), the microtubule associated
 CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
 CC neurofilament-F, presenilin 1, presenilin II, glial fibrillary acidic
 CC protein (GFAP), the cellular tumour antigen p53, B cell leukaemia/lymphoma
 CC protein-C (HMG-C) and neuroendocrine specific protein A.
 XX
 SQ Sequence 28 AA;

Query Match 100.0%; Score 140; DB 19; Length 28;
 Best local similarity 100.0%; Pred. No. 6.9e-16;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 RLEAKHRENVPGHERMGRGRTSSKELA 28

RESULT 3
 AAB99217
 ID AAB99217 standard; protein; 48 AA.
 XX
 AC AAB99217;
 XX
 DT 06-SEP-2001 (first entry)
 XX
 DE Beta-amyloid precursor protein, APP, protein fragment.
 XX
 KW Disease detection; age-related disease; Alzheimer's disease;
 KW Down's syndrome; cancer; neurodegenerative disease; Parkinson's disease;
 KW amyotrophic lateral sclerosis; Huntington's disease;
 KW spinocerebellar atrophy 3; multiple sclerosis; diabetes mellitus type II;
 KW degenerative disease; cardiovascular disease; rheumatoid arthritis;
 KW beta-amyloid precursor protein; APP.
 XX
 OS Unidentified.
 XX
 PN WO200140804-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 04-DEC-2000; 2000WO-NL000887.
 XX
 PR 03-DEC-1999; 99EP-0204140.
 XX
 PA (NEW-) KONINK NEDERLANDSE AKADEMIE VAN WETENSCHAPPE.
 XX
 PT Hol EM, Van Leeuwen FW;
 XX
 DR WPI; 2001-397965/42.
 XX
 PT Detecting a disease or pathological condition, associated with
 PT secretion of aberrant protein e.g. age-related diseases, by determining
 PT level of aberrant protein and/or its detectable part in body fluid
 PT and/or tissue -
 XX
 PS Examples; Fig 2; 36pp; English.

sequences in the genome and/or associated with the clearance of aberrant protein. The method comprises providing a sample of a body fluid and/or tissue of a patient and determining a level of the aberrant protein and/or its detectable part or the ratio between the two in the body fluid and/or tissue. The method enables diagnosing the disease before the patient exhibits clinical symptoms. The method is useful for diagnosing age-related diseases, preferably Alzheimer's disease, Down's syndrome or other age related diseases e.g. cancer; neurodegenerative diseases, such as frontal lobe dementia, progressive supranuclear palsy; and other diseases with abundant tau-positive filamentous lesions; Parkinson's disease, amyotrophic lateral sclerosis, Huntington's disease, spinocerebellar atrophy-3, multiple sclerosis; other inclusion body degenerative diseases such as cardiovascular diseases and rheumatoid arthritis. A number of other diseases which can be diagnosed are given in the specification. The present sequence is a fragment of the beta-amyloid precursor protein (APP), which was used in the examples from the present invention.

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CC

PT for treatment and prevention with specific ribozymes or wild-type RNA

XX Disclosure; Figure 20; 258pp; English.

XX This invention describes a novel method for the diagnosis of a disease caused by, or associated with, an RNA molecule that has a frameshift mutation. The method is used to diagnose age-related diseases, especially cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's disease, Down's syndrome, myotonic dystrophy, Huntington's disease, multiple sclerosis, alcholic liver disease, diabetes mellitus type II and many others listed) or susceptibility to these disorders. The method allows a definitive diagnosis of Alzheimer's disease in living patients, at an early stage. It is based on the observation that disease may be caused by mutations in RNA rather than DNA. The invention describes the use of neuronal system RNA molecules, specifically proteins including beta-amyloid precursor protein (beta-APP), the microtubule associated proteins tau and Tau, ubiquitin-B, apolipoprotein E, microtubule associated protein 2 (MAP2), neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic protein (GFAP), the cellular tumor antigen p53, B-cell leukaemia/lymphoma 2 (bcl-2) proto-oncogene, semaphorin III, Hupr-1, high mobility group protein-C (HMGPC) and neuroendocrine specific protein A.

XX SQ Sequence 28 AA:

Query	Match	Score	DB	Length
- Best Local Similarity	77.8%	Pred. No.	8.4e-09	28;
Matches	21;	Conservative	1;	Mismatches
QY	1	RLEAKHRENNVPGHERMGRGRSSKELA	27	5;
Db	2	RLEAKHRENNVQVMGRGRSSKELA	28	0;
				Gaps
				0;

RESULT 8

AY56393

ID AAY56393 standard; peptide: 17 AA.

XX

AC AAY56393;

XX

DT 15-FEB-2000 (first entry)

XX

DE Mutant beta-APP protein peptide sequence SEQ ID NO:3.

XX Mutant; beta-amyloid precursor protein; beta-APP; ubiquitin-B; vaccine; Alzheimer's disease; Down syndrome; T cellular immunity; neuroprotective; gene therapy.

XX

S Synthetic.

OS Homo sapiens.

XX

PN W0958564-A1.

XX

PD 18-NOV-1999.

XX

PR 30-APR-1999; 99WO-NO00141.

XX

PR 08-MAY-1998; 98NO-0002098.

XX

PA (NHYD) NORSK HYDRO AS.

XX

PI Gaudernack G, Eriksen JA, Moller M;

XX

PS WPI; 2000-039070/03.

XX

PT Frameshift mutant beta-amyloid precursor and ubiquitin-B peptides, useful for treating Alzheimer's disease and Down syndrome -

XX

PT Claim 10; Page 27; 33pp; English.

XX

CC The present invention describes frameshift mutant beta-amyloid precursor peptides (beta-APP) (AY56391 to AAY56394) and mutant ubiquitin-B

CC disease, amyotrophic lateral sclerosis, Huntington's disease, spinocerebellar ataxia-3, multiple sclerosis; other inclusion body diseases associated with ubiquitin, diabetes mellitus type II and other degenerative diseases such as cardiovascular diseases and rheumatoid arthritis. A number of other diseases which can be diagnosed are given in the specification. The present sequence is AMY 6 peptide, which was coupled to thyroglobulin by glutardialdehyde, and used to immunise rabbits for antibody production in the present invention. The AMY 6 peptide is a C-terminal fragment of the full-length beta-amyloid precursor protein (APP+1; mature APP and its signal peptide) protein.

SQ

Sequence 19 AA;

Query Match 58.9%; Score 82.5; DB 22; Length 19;
Best Local Similarity 94.8%; Pred. No. 1. 3e-06; Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 9 NYPGHERMGRGFFSSKELA 27
2 NVP-HERMGRGRTSSKELA 19

RESULT 10

AAB99215

ID AAB99215 standard; peptide: 14 AA.

XX

AC AAB99215;

XX

DT 06-SEP-2001 (first entry)

XX

DE AMY5 peptide.
KW AMY5; disease detection; age-related disease; Alzheimer's disease;
KW Down's syndrome; cancer; neurodegenerative disease; Parkinson's disease;
KW amyotrophic lateral sclerosis; Huntington's disease;
KW spinocerebellar ataxia-3; multiple sclerosis; diabetes mellitus type II;
KW degenerative disease; cardiovascular disease; rheumatoid arthritis;
KW beta-amyloid precursor protein; APP.

XX

OS Unidentified.

XX

PN WO200140804-A2.

XX

PD 07-JUN-2001.

XX

PP 04-DEC-2000; 2000WO-NL00887.

XX

PR 03-DEC-1999; 99EP-0204140.

XX

(NEWW-) KONINK NEERLANDSE AKAD VAN WETENSCHAPPE.

XX

PI Hol EM, Van Leeuwen FW;

XX

DR WPI; 2001-397965/42.

XX

PT Detecting a disease or pathological condition, associated with secretion of aberrant protein e.g. age related diseases, by determining level or aberrant protein and/or its detectable part in body fluid and/or tissue

XX

PS Disclosure; Page 24; 36pp; English.

XX

The present invention relates to a method for detecting a disease or pathological condition associated with molecular misreading of coding sequences in the genome and/or associated with the clearance of aberrant protein. The method comprises providing a sample of a body fluid and/or tissue of a patient and determining a level of the aberrant protein and/or its detectable part or the ratio between the two in the body fluid and/or tissue. The method enables diagnosing the disease before the patient exhibits clinical symptoms. The method is useful for diagnosing age-related diseases, preferably Alzheimer's disease, Down's syndrome or other age related diseases e.g. cancer; neurodegenerative diseases, such as frontal lobe dementia, progressive supranuclear palsy; and other

CC diseases with abundant tau positive filamentous lesions, Parkinson's disease, amyotrophic lateral sclerosis, Huntington's disease, spinocerebellar ataxia-3, multiple sclerosis; other inclusion body diseases associated with ubiquitin, diabetes mellitus type II and other degenerative diseases such as cardiovascular diseases and rheumatoid arthritis. A number of other diseases which can be diagnosed are given in the specification. The present sequence is AMR 5 peptide, which was coupled to thyroglobulin by glutardialdehyde, and used to immunise rabbits for antibody production in the present invention. The AMR 5 peptide is a C-terminal fragment of the full-length beta-amyloid precursor protein (APP+1; mature APP and its signal peptide) protein.

SQ

Sequence 14 AA;

Query Match 45.0%; Score 63; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0. 0015; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 RMGRGRGRTSSKELA 27
2 RMGRGRGRTSSKELA 14

RESULT 11

AAV56394

ID AAV56394 standard; peptide; 12 AA.

XX

AC AAV56394;

XX

DT 15-FEB-2000 (first entry)

XX

DE Mutant beta APP protein peptide sequence SEQ ID NO:4.

XX

KW Mutant; beta-amyloid precursor protein; beta-APP; ubiquitin-B; vaccine; Alzheimer's disease; Down syndrome; T cellular immunity; neuroprotective; gene therapy.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9958564-A1.

XX

PD 18-NOV-1999.

XX

PP 30-APR-1999; 99WO-NO00141.

XX

PR 08-MAY-1998; 99NO-0002098.

XX

(NHYD) NORSK HYDRO AS.

XX

PI Gaudernack G, Eriksen JA, Moller M;

XX

DR WPI; 2000-039070/03.

XX

PT Farnesyl mutant beta-amyloid precursor and ubiquitin-B peptides, useful for treating Alzheimer's disease and Down syndrome

XX

PS Claim 10; Page 27; 33pp; English.

XX

The present invention describes farnesyl mutant beta-amyloid precursor peptides (beta-APP) (AAV56394 to AAV56395) associated with Alzheimer's disease and Down syndrome eliciting T cellular immunity. The peptides may be used as a vaccine for Alzheimer's disease and Down syndrome. The vaccination is sufficient to induce specific T-cell immunity to mutant beta-APP and/or UbB peptides that are associated with Alzheimer's disease or Down syndrome. The patient may be stimulated in vivo or ex vivo with the peptides. The peptides and DNA encoding the peptides can also be used for the treatment or prophylaxis of Alzheimer's disease or the treatment of Down syndrome.

XX

SQ Sequence 12 AA;

Query Match 41.4%; Score 58; DB 21; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0085; Mismatches 0;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 MGRGRSSKELA 27
 Db 1 MGRGRSSKELA 12

RESULT 12
 AAU46738
 ID AAU46738 standard; Protein: 57 AA.
 XX
 AC AAU46738;
 XX
 DN 27-FEB-2002 (first entry)
 XX
 DE Propionibacterium acnes immunogenic protein #7634.
 XX
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX
 OS Propionibacterium acnes.
 XX
 PN WO200181581-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 20-APR-2001; 2001WO-US12865.
 XX
 PR 21-APR-2000; 2000US-199047P.
 PR 02-JUN-2000; 2000US-208841P.
 PR 07-JUL-2000; 2000US-216747P.
 XX
 PA (CORT-) CORIXA CORP.
 XX
 PI Skeiky Yaw, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 XX
 DR WPI; 2001-616747/71.
 DR N-PSDB; AAS59535.

XX
 PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris -
 XX
 S Example 1; SEQ ID No 7933; 1069pp; English.

CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at [ftp://wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).
 XX Sequence 57 AA;

Query Match 36.4%; Score 51; DB 22; Length 57;
 Best Local Similarity 81.8%; Pred. No. 0.73; Mismatches 0;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 VPGHERMGRGR 20
 Db 47 VPGHRTGGR 57

RESULT 13
 AAU6292
 ID AAU6292 standard; Protein: 57 AA.
 XX
 AC AAU6292;
 XX
 DN 27-FEB-2002 (first entry)
 XX
 DE Propionibacterium acnes immunogenic protein #27188.
 XX
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX
 OS Propionibacterium acnes.
 XX
 PN WO200181581-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 20-APR-2001; 2001WO-US12865.
 XX
 PR 21-APR-2000; 2000US-199047P.
 PR 02-JUN-2000; 2000US-208841P.
 PR 07-JUL-2000; 2000US-216747P.
 XX
 PA (CORT-) CORIXA CORP.
 XX
 PI Skeiky Yaw, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 XX
 DR WPI; 2001-616747/71.
 DR N-PSDB; AAS59726.

XX
 PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris -
 XX
 PS Example 1; SEQ ID No 27487; 1069pp; English.

CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at [ftp://wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).
 XX Sequence 57 AA;

Query Match 36.4%; Score 51; DB 22; Length 57;
 Best Local Similarity 81.8%; Pred. No. 0.73;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0; .

Oy 10 VPGHERRMGGR 20
 ||||| |||||
 Db 47 VPGHRRTGGR 57

RESULT 14

ABB59130 36.4%; Score 51; DB 22; Length 57;
 Best Local Similarity 81.8%; Pred. No. 0.73;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0; .

ID ABB59130 standard; Protein; 491 AA.
 XX
 AC EP592106-A1.
 XX
 AC 13-APR-1994.
 XX
 DT 07-SEP-1993; 93EP-0307051.
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 4182.
 XX
 Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
 XX
 Drosophila melanogaster.
 OS
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PR 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 XX
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 PT WPI; 2001-656860/75.
 DR N-PSDB; ABL03232.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions .
 XX
 PS Disclosure: SEQ ID NO 4182; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB0116176-AB0130511), expressed DNA sequences (ABL0184-ABL16175) and the encoded proteins (ABB5737-ABB72072).
 CC The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 491 AA;

Query Match 36.1%; Score 50.5; DB 22; Length 491;
 Best Local Similarity 48.0%; Pred. No. 11; Mismatches 3; Indels 7; Gaps 1;

Matches 12; Conservative 3; Mismatches 3; Indels 7; Gaps 1;

Oy 10 VPGHERRMGGR 27
 ||||| |||||
 Db 171 LPSPHERLIGLRSLSOFTIELKELA 195

RESULT 15

AAR52350 36.4%; Score 51; DB 22; Length 57;
 Best Local Similarity 81.8%; Pred. No. 0.73;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0; .

ID AAR52350 standard; Peptide; 26 AA.
 XX

AC AAR52350;
 XX 30-SEP-1996 (first entry)
 DT XX
 DE XX
 KW XX
 KW antibody; humanised; murine; human; heavy chain; light; variable; framework region; complementarity determining region; reshaping; modelling; surface residue; modify.
 KW XX
 OS XX
 PN XX
 PR EP592106-A1.
 XX
 PD 13-APR-1994.
 XX
 PR 09-SEP-1992; 92US-0942245.
 XX
 PA (PEDE/) PEDERSEN J T.
 PA (IMMU-) IMMUNOGEN INC.
 XX
 PT Guild BC, Pedersen JT, Rees AR, Roguska MA, Searle SMJ;
 XX
 DR WPI; 1994-120230/15.
 XX
 PT Method of resurfacing of rodent antibodies to produce humanised antibody forms - for producing non-human antibodies with improved therapeutic efficiency by presenting human surface on V-region
 PT XX
 PS XX
 CC Modification of a rodent antibody or fragment by resurfacing in order to produce a humanised rodent antibody can be determined by calculating the homology between murine and human antibody surfaces. In order to test the resurfacing approach of the invention, three humanisation experiments were set up. (1) traditional loop grafting; (2) resurfacing approach using most similar chain; and (3) resurfacing approach using human sequences with most similar surface residues. AAR52243-447 are the surface residue patterns in mouse heavy chain antibodies variable regions. These "patches" were used in the third method, where rodent light and heavy chains were matched and the most similar human sequence found independently only over the surface residues indicated in AAR5203-67.
 CC XX
 SQ Sequence 26 AA;

Query Match 35.7%; Score 50; DB 15; Length 26;
 Best Local Similarity 45.0%; Pred. No. 0.43;
 Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Oy 3 EAKHRENVPGHERRMGGR 22
 ||||| : ||||| : |||||
 Db 5 EVRPGKGTTPGHKEKKGSSTS 24

Search completed: October 29, 2002, 13:59:23
 Job time : 32 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 29, 2002, 13:55:48 ; Search time 43 Seconds

Perfect score: 140

Sequence: 1 RLEAKHENVPGHMRGRTSSKELA 27

Scoring table: BLOSUM62

Gapopen 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database :

PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

RESULT 1

H82989 conserved hypothetical protein PA5246 [imported] - *Pseudomonas aeruginosa* (strain PAO

C;Species: *Pseudomonas aeruginosa*

C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C;Accession: H82989

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.;

Adman, S.; Yuan, Y.; Brady, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L

; Iony, S.; Olson, M.V.

Nature 405, 955-954, 2000

A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pa

A;Reference number: A82950; PMID:20437337; PMID:10984043

A;Accession: H82989

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-157 <STO>

A;Cross-references: GB:A8004937; GB:AE004091; NID:99951553; PIDN:AAG08631.1; GSPDB:GN

A;Experimental source: strain PA01

C;Genetics:

A;Gene: PA5246

Result No.: Score Query Match Length DB ID

No.: Description

1 54.5 38.9 157 2 H82989 conserved hypothetical protein

2 50.35.7 72 2 A86664 hypothetical prote

3 50.35.7 229 2 H82043 quanylate kinase V

4 49.5 35.4 424 2 T39524 hypothetical prote

5 49.5 35.4 2140 2 T18543 probable cell-adhe

6 49.35.0 829 2 AH282 hypothetical prote

7 48 34.3 244 JCT801 dendritic cell-ass

8 48 34.3 962 2 A81817 translation initia

9 48 34.3 962 2 C81060 deacetoxycephalospi

10 47.5 33.9 332 2 A29711 probable aspartate

11 46.5 33.2 382 2 T35706 competence regulat

12 46.5 33.2 769 2 A33848 two-component sens

13 46 33.2 769 2 B65604 oligopeptide trans

14 46 32.9 302 2 AB3573 homolog of cell di

15 46 32.9 342 2 A97325 probable transmemb

16 46 32.9 485 2 T35663 hypothetical prote

17 46 32.9 614 2 F96791 hypothetical prote

18 46 32.9 650 2 T32897 ribonuclease

19 46 32.9 898 2 H87481 serine/threonine-s

20 46 32.9 1064 2 S52687 amideide sensitiv

21 46 32.9 1420 1 A44361 SRY protein homolo

22 45 32.1 79 2 S22082 insulin-like growth

23 45 32.1 155 1 IGB02 insulin-like growth

24 45 32.1 179 2 S04858 DNA-binding protei

25 45 32.1 240 2 H90778 hypothetical prote

26 45 32.1 242 2 C85640 hypothetical prote

27 45 32.1 403 2 H87569 probable membrane

28 45 32.1 1245 2 S55259 lysobactin synthet

29 32.1 1575 2 T18545

ribulose-biphosph
laccase (EC 1.10.3
hypothetical prote
probable iron-type
ferric enterobacti
hypothetical prote
probable ribosomal
electron transfert
related to COpL-in
replication licens
histidine-rich cal
probable phospholi
hypothetical prote
nonstructural poly
30S ribosomal prot
DEAD-box RNA helic

Score	31.8	41.4	2	AG197
DB	44.5	31.1	1	KSASTL
Length	31.8	60.9	1	KSASTL
Indels	32	44	144	T49745
Mismatches	33	44	215	T49743
Matches	34	44	306	F84405
Score	35	44	314	H89884
DB	36	44	326	T40353
Length	37	44	407	G90453
Indels	38	44	532	T49457
Mismatches	39	44	586	E69314
Score	40	44	852	A34373
DB	41	44	314	T09344
Length	42	44	946	A96748
Indels	43	44	314	S72351
Mismatches	44	44	311	E8113
Score	45	43.5	311	T34592

QY 11 PGHERMGRGRTSSKE 25
 | ||:||:| | | :| |
 46 PDHEKMGKGTLSSE 60

RESULT 3
 H82043 guanylate kinase VC2708 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)
 C;Species: *Vibrio cholerae*
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C;Accession: H82043
 R;Heidelberg, J.F.; Elson, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
 chardson, D.; Ermlaeva, M.D.; Yamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, E.;
 I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
 A;Reference number: A82035; MUID:20400833; PMID:10952301
 A;Accession: H82043
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-129 <HEI>
 A;Cross-references: GB:AE004336; GB:AF003852; NID:9657296; PIDN:AAF95848.1; GSPDB:GN001
 A;Experimental source: serogroup O1; strain N16961; biotype El Tor
 C;Genetics:
 A;Gene: VC2708
 A;Map position: 1
 C;Superfamily: guanylate kinase; guanylate kinase homology

Query Match 35.7%; Score 50; DB 2; Length 229;
 Best Local Similarity 47.4%; Pred. No. 7.1;
 Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 1 RLEFKHENVPGHMRGK 19
 | | :| | | :| | | :| |
 Db 8 RLQRHNRNLNSGEGESMGK 26

RESULT 4
 T39524 hypothetical protein SPRC1685.08 - fission yeast (*Schizosaccharomyces pombe*)
 C;Species: *Schizosaccharomyces pombe*
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C;Accession: T39524
 R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Duesterhoeft, A.
 submitted to the EMBL Data Library, July 1998
 A;Reference number: Z22861
 A;Accession: T39524
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-829 <KUR>
 A;Cross-references: GB:BA000019; PIDN:BAE75514.1; PID:g17132949; GSPDB:GN00179
 A;Experimental source: strain PCC 7120
 C;Genetics:
 A;Gene: alr3815

Query Match 35.0%; Score 49; DB 2; Length 829;
 Best Local Similarity 45.0%; Pred. No. 36;
 Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 QY 7 RENVPGHMRGRTSSKE 26
 Db 704 RENTPGYNLIGDITLNRPL 723

RESULT 7
 JC7801 dendritic cell-associated nuclear protein 1, DCNPI - human
 C;Species: *Homo sapiens* (man)
 C;Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 03-Jun-2002
 C;Accession: JC7801
 R;Masuda, M.; Senju, S.; Fujii, S.; Terasaki, Y.; Takeya, M.; Hashimoto, S.; Matsushi
 Biochem. Biophys. Res. Commun. 290, 1022-1029, 2002
 A;Title: Identification and immunocytochemical analysis of DCNPI, a dendritic cell-as
 A;Reference number: JC7801; PMID:1179817; MUID:21656978
 A;Accession: JC7801
 A;Molecule type: mRNA
 A;Residues: 1-244 <MAS>
 A;Cross-references: DBP:AB074498
 C;Comment: This protein is a dendritic cell-associated nuclear membrane protein invol
 A;Gene: dcnp1
 A;Map position: 5

Query Match 34.3%; Score 48; DB 2; Length 244;
 Best Local Similarity 66.7%; Pred. No. 15;
 C;Species: *Lentinula edodes* (shiitake mushroom)
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
 C;Accession: T18543

RESULT 5
 T18543 probable cell-adhesion protein MRB1 - shiitake mushroom
 C;Species: *Lentinula edodes* (shiitake mushroom)
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
 C;Accession: T18543

R;Kondoh, O.; Muto, A.; Kajiwara, S.; Takagi, J.; Saito, Y.; Shishido, K.
 Gene 154, 31-37, 1995
 A;Title: A fruiting body-specific cDNA, mfbac, from the mushroom *Lentinus edodes* enc
 A;Reference number: Z18660; MUID:9512398; PMID:7867945
 A;Accession: T18543
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-2140 <KON>
 A;Cross-references: EMBL:D14487; NID:91906308; PIDN:BAA18903.1; PID:g1906309
 A;Experimental source: strain FMC2
 C;Genetics:
 A;Gene: MRB1

Query Match 35.4%; Score 49.5; DB 2; Length 2140;
 Best Local Similarity 33.3%; Pred. No. 80;
 Matches 12; Conservative 6; Mismatches 7; Indels 11; Gaps 1;
 QY 3 EAKHENVVRGH-----ERNGRGRGTTSSKLA 27
 Db 159 EAKDKENLPDHWCWECOPSSLERIDREKRSIQIA 194

Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 8 ENVPOGHERMGRG 19

C;Species: *Neisseria meningitidis* (strain N)

C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001

C;Accession: A81817

A81817 translation initiation factor IF-2 NMA1897 [similarity] - *Neisseria meningitidis* (strain N)C;Species: *Neisseria meningitidis* (strain N)

C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 19-May-2000

C;Accession: A29711; A41864

R;Samson, S.M.; Dotzlar, J.E.; Slisz, M.L.; Becker, G.W.; Van Frank, R.M.; Veal, L.E.

Bio/Technology 5, 1207-1214, 1987

A;Title: Cloning and expression of the fungal expandase/hydroxylase gene involved in

A;Reference number: A81817

A;Accession: A81817

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-962 <PAR>

A;Cross-references: GB:AL162757; GB:AL157959; NID:97380371; PIDN:CAB85118.1; PID:9738053

A;Experimental source: serogroup A, strain 22491

C;Genetics:

C;Gene: infB; NMA1897

C;superfamily: translation initiation factor IF-2; translation elongation factor Tu homolog

FJ465-574/Domain: translation elongation factor Tu homology <ETU>

Query Match 34.3%; Score 48; DB 2; Length 962; Best Local Similarity 40.9%; Pred. No. 59; Mismatches 4; Indels 9; Conservative 9; Gaps 0;

QY 3 EAKHRENVPGHERMGRGRTSSK 24

Db 195 EPKEAKAPKHERNGKDKK 216

RESULT 9

C81060 translation initiation factor IF-2 NMB1643 [imported] - *Neisseria meningitidis* (strain N)C;Species: *Neisseria meningitidis* (strain N)

C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001

C;Accession: C81060

R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.

Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;

Ri, H.; Qin, H.; Vaishnav, J.; Gill, J.; Scarlato, V.; Masignani, V.; Plaza, M.

Science 287, 1809-1815, 2000

A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; ve

A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.

A;Accession number: A81000; MUND:20175755; PMID:10710307

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-962 <ETU>

A;Cross-references: GB:AE002514; GB:AE002098; NID:97226886; PIDN:AAF41992.1; PID:9722689

A;Experimental source: serogroup B, strain MC58

C;Genetics:

A;Gene: NMB1643

C;Superfamily: translation initiation factor IF-2; translation elongation factor Tu homolog

FJ465-574/Domain: translation elongation factor Tu homology <ETU>

Query Match 34.3%; Score 48; DB 2; Length 962; Best Local Similarity 40.9%; Pred. No. 59; Mismatches 4; Indels 9; Conservative 4; Gaps 0;

QY 3 EAKHRENVPGHERMGRGRTSSK 24

Db 195 EPKEAKAPKHERNGKDKK 216

RESULT 10

A29711

deacetoxypephalosporin C synthetase - fungus (*Acremonium* sp.)

N;Alternate names:

expandase; hydroxylase

C;Species: *Acremonium* sp.

C;Date: 23-Oct-1980 #sequence_revision 31-Dec-1988 #text_change 19-May-2000

C;Accession: A29711

R;Samson, S.M.; Dotzlar, J.E.; Slisz, M.L.; Becker, G.W.; Van Frank, R.M.; Veal, L.E.

Bio/Technology 5, 1207-1214, 1987

A;Title: Cloning and expression of the fungal expandase/hydroxylase gene involved in

A;Reference number: A29711

A;Status: not compared with conceptual translation

A;Accession: A29711

A;Molecule type: DNA

A;Residues: 1-332 <SAM>

A;Note: the source is designated as *Cephalosporium acremonium*

C;superfamily: 1-aminoacyclopropane-1-carboxylate oxidase

Query Match 33.9%; Score 47.5; DB 2; Length 332; Best Local Similarity 55.0%; Pred. No. 24; Mismatches 11; Conservative 2; Indels 6; Gaps 1; Gaps 1;

QY 5 KHRHENVPGH-ERMGRCRTSS 23

Db 243 KHRVKSPPGRDQVRGSSRTSS 262

RESULT 11

T35705

probable aspartate transaminase (EC 2.6.1.1) SC7H1.11 [similarity] - *streptomyces* coeC;Species: *Streptomyces coelicolor*

C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 20-Jun-2000

C;Accession: T35706

R;Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, January 1998

A;Reference number: Z21548

A;Accession: T35706

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Residues: 1-382 <NUR>

A;Cross-references: EMBL:AL021411; PIDN:CAA16198.1; GSPDB:GN00070; SCOEDB:SC7H1.11

A;Experimental source: strain A3(2)

C;Genetics:

A;Gene: SCOEDB:SC7H1.11

C;Superfamily: aspartate transaminase

C;Keywords: aminotransferase

Query Match 33.2%; Score 46.5; DB 2; Length 382; Best Local Similarity 46.2%; Pred. No. 39; Mismatches 12; Conservative 1; Indels 7; Gaps 1;

QY 3 EAKHRENVPGHERMGRGRTSSK 21

Db 197 EAVHLAYVPGEHPSALEIESLRQRT 222

RESULT 12

A35848

C;Species: *Bacillus subtilis*

C;Date: 23-Oct-1990 #sequence_revision 23-Oct-1990 #text_change 15-Oct-1999

C;Accession: A35848

R;Weinrauch, Y.; Penchev, R.; Dubnau, E.; Smith, I.; Dubnau, D.

Genes Dev. 4, 860-872, 1990

Copyright (c) 1993 - 2002 Compugen Ltd.	GenCore version 5.1.3	
OM protein - protein search, using sw model.		
Run on: October 29, 2002, 13:55:48 ; Search time 34 Seconds		
Sequence: (without alignments)		
Scoring table: BLOSUM52		
Gpop 10.0 , Gapext 0.5		
Searched: 112892 seqs, 41476328 residues		
total number of hits satisfying chosen parameters: 112892		
Minimum DB seq length: 0		
Maximum DB seq length: 200000000		
Post-processing: Minimum Match 0%		
Maximum Match 100%		
Listing first 45 summaries		
Database : Swissprot-40:*		
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		
SUMMARIES		
Result No.	Score	Query Match Length DB ID
1	55	39.3 576 1 LEI2_RALSO
2	47.5	33.9 332 1 EXPR_CEPAC
3	46.5	33.2 769 1 KINI_YEAST
4	46	32.9 1064 1 AXK_XENLA
5	46	32.9 1074 1 IGF2_BOVIN
6	45	32.1 155 1 IGF2_SHEEP
7	45	32.1 179 1 RCA_ANAB
8	44.5	31.8 414 1 RAL_NECR
9	44.5	31.8 609 1 LACILEMENT
10	44	31.4 220 1 SRY_CANFA
11	44	31.4 539 1 DOP2_DROME
12	44	31.4 852 1 SMC_RABBIT
13	44	31.4 858 1 PDG1_ARATH
14	44	31.4 1093 1 RNTL_NECR
15	43.5	31.1 206 1 RSL_PSEAE
16	43	30.7 151 1 GDF7_MOUSE
17	43	30.7 181 1 IGF2_PIG
18	43	30.7 201 1 H2Z3_SCHPO
19	43	30.7 206 1 CASL_PIG
20	43	30.7 208 1 SRY_PIG
21	43	30.7 285 1 CAB_TWIV
22	43	30.7 855 1 CLOC_MOUSE
23	43	30.7 1944 1 CHD3_HUMAN
24	42.5	30.4 415 1 RCA_ANASC
25	42.5	30.4 758 1 VKGC_BOVIN
26	42	30.0 95 1 VESB_BP4
27	42	30.0 355 1 VEGA_RHOA
28	42	30.0 356 1 GLN2_SOBN
29	42	30.0 356 1 RECA_PARDE
30	42	30.0 406 1 VBB6_AQURE
31	42	30.0 687 1 TRA_HAEN
32	42	30.0 751 1 A4_SAISC
33	42	30.0 770 1 AA_HUMAN
ALIGNMENTS		
Query Match	39.3%	Score 55; DB 1; Length 576;
Result ID	LEI2_RALSO	STANDARD; PRT; 576 AA.
DB	08XZ5;	
DT	15-JUN-2002 (Rel. 41, Last sequence update)	
DT	15-JUN-2002 (Rel. 41, last annotation update)	
DE	2-isopropylmalate synthase 2 (EC 4.1.3.12) [Alpha-isopropylmalate synthase 2] (Alpha-IPM synthetase 2).	
GN	LEU2 OR RSP0322 OR RSP0545	
OS	Ralstonia solanacearum (Pseudomonas solanacearum).	
OG	Plasmid megaplasmid.	
OC	Bacteria; Proteobacteria; beta subdivision; Ralstonia group; Ralstonia.	
OX	NCBI_TaxID:305;	
RP	[1]	
RC	SEQUENCE FROM N A.	
RX	STRAIN:GM1000; MEDLINE=21681879; PubMed=11823852;	
RA	Salamoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattoilico L., Chandler M., Choisne N., Claudet-Benard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saunin W., Schilex T., Siguer P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415:497-502(2002).	
RL	-1- FUNCTION: Catalyzes the condensation of the acetyl group of acetyl-CoA with 3-methyl-2-oxobutanate (2-oxoisovalerate) to form 3-carboxy-3-hydroxy-4-methylpentanate (2-isopropylmalate).	
CC	-1- CATALYTIC ACTIVITY: 3-carboxy-3-hydroxy-4-methylpentanate + CoA = acetyl-CoA + 3-methyl-2-oxobutanate + H(2)O.	
CC	-1- PATHWAY: Leucine biosynthesis; first step.	
CC	-1- SUBUNIT: Homotetramer (By similarity).	
CC	-1- SIMILARITY: BELONGS TO THE ALPHA-IPM SYNTHETASE / HOMOCITRATE SYNTHASE FAMILY. LEU2 2 SUBFAMILY.	
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CC	EMBL; AL646078; CAD1743; 1; PROST1; PS00815; AIPM_HOMOCIT_SYNTH_1; PROST1; PS00816; AIPM_HOMOCIT_SYNTH_2; 1; Leucine biosynthesis; Lyase; Plasmid; Complete proteome.	
DR	InterPro; IPR002034; AIPM_HcItt; HMGU-like.	
DR	Pfam; PF00682; HMGU-like_1.	
DR	TIGR47; TIGR0970; LeuA_yeast; 1; PROST1; PS00815; AIPM_HOMOCIT_SYNTH_1; 1; PROST1; PS00816; AIPM_HOMOCIT_SYNTH_2; 1; Leucine biosynthesis; Lyase; Plasmid; Complete proteome.	
KW	SEQUENCE 576 AA; 3149 MW; BBCR0A9A66BA332B CRC64;	
SQ	P05067 homo sapien	

CC	RL	Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.	
DR	CC	-1- FUNCTION: THIS PROTEIN IS PROBABLY A SERINE/THREONINE PROTEIN KINASE.	
EMBL; Z43932; CAB07903; 1;	CC	KINASE.	
DR	CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.	
EMBL; Z39120; CAB1515; 1;	CC	NIMI SUBFAMILY.	
DR	CC		
EMBL; M22856; AAAC2319; 1;	CC		
DR	CC		
EMBL; M11283; AA22324; 1;	CC		
DR	CC		
PIR; A35848; A35848; comp.	CC		
DR	CC		
Sublist: BG10380; InterPro: IPR003394; AtPbind_Atpase.	CC		
DR	CC		
InterPro: IPR043559; HIS_KIN_Sig.	CC		
DR	CC		
Pfam: PF02518; HATpase_c; 1.	CC		
DR	CC		
SMART; SM00367; HATpase_c; 1.	CC		
DR	CC		
PROSITE: PS500109; HIS_KIN; 1.	CC		
KW	CC		
Sensory transduction; Phosphorylation; Transferase; Kinase;	CC		
KW	CC		
Transmembrane; Complete proteome.	CC		
DOMAIN	1		
FT	TRANSMEM	10	
FT	DOMAIN	34	
FT	TRANSMEM	114	
FT	DOMAIN	135	
FT	TRANSMEM	145	
FT	DOMAIN	168	
FT	TRANSMEM	236	
FT	DOMAIN	258	
FT	TRANSMEM	273	
FT	DOMAIN	296	
FT	TRANSMEM	300	
FT	DOMAIN	323	
FT	TRANSMEM	338	
FT	DOMAIN	358	
FT	TRANSMEM	362	
FT	DOMAIN	384	
FT	TRANSMEM	388	
FT	DOMAIN	571	
FT	TRANSMEM	579	
FT	MOD_RES	456	
FT	CONFLICT	604	
FT	CONFLICT	610	
FT	CONFLICT	628	
FT	CONFLICT	636	
FT	SEQUENCE	769 AA;	
QY	1	RL	LEAKHRENVPGERMGGR-TSKEL 26
Db	649	KLVAHEQERVPPFIRLNTRGRTASLDL 675	
RESULT 4			
ID	KINL_YEAST	STANDARD;	PRT; 1064 AA.
AC	P13185; Q04606;		
DT	01-NOV-1997 (Rel. 35, last sequence update)		
DT	01-NOV-1990 (Rel. 13, Created)		
DE	Protein kinase KINL (EC 2.7.1.-).		
GN	KINL OR YDR122W OR YD9727.17.		
OS	Saccharomyces cerevisiae (Baker's yeast).		
OC	Bukaryota; Fungi; Ascomycota; Saccharomycetidae; Saccharomycetes.		
OC	Saccharomycetidae; Saccharomycetaceae; Saccharomyces.		
OX	NCBI_TAXID=4932;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MLINE=8731789; PubMed=2957690;		
RX	Levin D.E., Hammond C.T., Raiston R.O., Bishop J.M.,		
RX	Proc. Natl. Acad. Sci. U.S.A. 84:6035-6039(1987).		
RX	[2]		
RP	SEQUENCE FROM N.A.		
RX	STRAIN=S288C / AB972;		
RX	Murphy L., Shore L., Harris D., Barrell B.G., Rajandream M.A.,		
RA	Walsh S.V.;		
RESULT 5			
ID	APX_XENLA	STANDARD;	PRT; 1420 AA.
AC	Q01613;		
DT	01-JUN-1994 (Rel. 29, Created)		
DT	01-JUN-1994 (Rel. 29, Last sequence update)		
DT	15-JUL-1998 (Rel. 36, Last annotation update)		
DE	Apical protein (APX).		
GN	APX.		
OS	Xenopus laevis (African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;		
OC	Xenopodinae; Xenopus.		
OX	NCBI_TAXID=8355;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Ovary;		
RX	MLINE=93107151; PubMed=1334959;		
RA	Staub O., Verrey F., Kleymann T.R., Benos D.J., Rossier B.C., Krahenbuhl J.-P.;		

RT "Primary structure of an apical protein from *Xenopus laevis* that participates in amiloride-sensitive sodium channel activity.";
 RT RL J. Cell Biol. 119:1497-1506(1992).

RT -!- FUNCTION: IS PART OF A MULTIMERIC COMPLEX WHICH IS INVOLVED IN AMILORIDE-SENSITIVE SODIUM CHANNEL ACTIVITY.

CC CC -!- SUBCELLULAR LOCATION: Membrane-associated.

CC CC -!- TISSUE SPECIFICITY: KIDNEY, PROXIMAL INTESTINE, OOCYTES, AND TO A LESSER EXTENT IN THE DISTAL INTESTINE, STOMACH AND EYE.

CC CC -!- SIMILARITY: SOME, TO HUMAN APXL.

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CC DR EMBL; Z14997; CAA78718.1; -.

CC PIR; S25517; S25517.

CC PIR; A44361; A44361.

CC Membrane; Sodium transport; transport.

FT DOMAIN 111 114 POLY-SER.

FT DOMAIN 559 564 POLY-SER.

FT DOMAIN 1048 1051 POLY-THR.

FT SEQUENCE 1420 AA; 159467 MW; ODD8B5C11413FFBC CRC64;

Query Match 32.9%; Score 46; DB 1; Length 1420; Best Local Similarity 38.1%; Pred. No. 72; Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps 0; Db 149 INMKHKQNPNKHAYGLQRNS 169

RESULT 6

IGF2_BOVIN STANDARD; PRT; 155 AA.

ID IGF2_BOVIN STANDARD; PRT; 155 AA.

AC P07456; P07456;

DR 01-APR-1988 (Rel. 07, Created)

DR 01-MAY-1992 (Rel. 22, Last sequence update)

DR 01-FEB-1996 (Rel. 33, Last annotation update)

DE Insulin-like growth factor II precursor (IGF-II) (Erythrotropin) (Fragment).

DE IGF2.

OS Bos taurus (Bovine).

OC Bovaria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1] SEQUENCE OF 6-155 FROM N.A.

RR TISSUE=Liver;

RC MEDLINE=90356421; PubMed=2388846;

RA Brown, W.M., Dziegielewska, K.M., Foreman, R.C., Saunders, N.R.; RT The nucleotide and deduced amino acid sequences of insulin-like growth factor II cDNAs from adult bovine and fetal sheep liver. Nucleic Acids Res. 18:4614-4614(1990).

RN [2] SEQUENCE OF 6-62 FROM N.A.

RR MEDLINE=93083057; PubMed=1280544;

RA Congote, L.F., Mazza, L., Palffy, R.G.E.; RT Nucleotide sequence of the central coding region of bovine erythropoietin/insulin-like growth factor II cDNA from fetal intestine and northern analysis of the major IGF II transcripts at the time of hepatic erythropoiesis. Comp. Biochem. Physiol. 103B:127-131(1992).

RN [3] SEQUENCE OF 1-67; MEDLINE=86088881; PubMed=3941093;

RA Honegger, A.; Humber, R.E.; RT "Insulin-like growth factors I and II in fetal and adult bovine

RT serum. Purification, primary structures, and immunological cross-reactivities."; RL J. Biol. Chem. 261:569-575(1986).

CC [4] REVISITONS.

CC RX Francis, G.L., Upton, F.M., Ballard, F.J., McNeil, K.A., Wallace, J.C.; CC "Insulin-like growth factors 1 and 2 in bovine colostrum. Sequences and biological activities compared with those of a potent truncated form."; RL Biochem. J. 251:95-103(1988).

CC DR EMBL; X53553; CAA37861.1; -.

CC PIR; B25623; IGB02.

CC PIR; A34645; A34645.

CC PIR; S00466; S00466.

CC PIR; S10983; S10983.

CC HSPB; P01344; 1692.

CC DR InterPro; IPR004825; Ins/IGF/relax.

CC DR Pfam; PF00049; Insulin; 1.

CC DR PROSITE; PS00262; INSULIN_1.

CC DR PROSITE; SM00078; IIGF; 1.

CC KW Insulin family; Mitogen; Growth factor.

FT CHAIN 1 1 INSULIN-LIKE GROWTH FACTOR II.

FT DOMAIN 1 28 B.

FT DOMAIN 29 40 C.

FT DOMAIN 41 61 A.

FT DOMAIN 62 67 D.

FT PROPEP 68 155 E PEPTIDE.

FT DISULFID 9 47 BY SIMILARITY.

FT DISULFID 21 60 BY SIMILARITY.

FT DISULFID 46 51 BY SIMILARITY.

FT CONFLICT 22 23 GD -> DG (IN REF. 5).

FT CONFLICT 35 35 I -> S (IN REF. 3).

FT SEQUENCE 155 AA; 17261 MW; 50A453549397EOF CRC64;

Query Match 32.1%; Score 45; DB 1; Length 155; Best local Similarity 50.0%; Pred. No. 10; Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0; Db 103 RAGLPLATLRAAGRGTAKEL 122

RESULT 7

IGF2_SHEEP STANDARD; PRT; 179 AA.

ID IGF2_SHEEP STANDARD; PRT; 179 AA.

AC P10764;

DT	01-JUL-1989 (Rel. 11, Created)
DT	01-OCT-1989 (Rel. 12, last sequence update)
DT	01-OCT-1996 (Rel. 34, last annotation update)
DE	Insulin-like growth factor II precursor (IGF-II).
GN	IGF2.
OS	Ovis aries (Sheep).
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae; Ovis.
OC	Bovidae; Caprinae; Ovis.
OX	NCBI_TaxID=3940;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Liver;
RX	MEDLINE=69345107; PubMed=2762134;
RA	O Mahoney J V., Adams T.E.;
RT	"Nucleotide sequence of an ovine insulin-like growth factor-II cDNA.";
RL	Nucleic Acids Res. 17:5392-5392(1989).
RN	[2]
RP	SEQUENCE FROM N.A.
RA	TISSUE=Liver;
RT	MEDLINE=90356421; PubMed=2388846;
RA	Brown W.M., Dziegielewska K.M., Foreman R.C., Saunders N.R.;
RT	"The nucleotide and deduced amino acid sequences of insulin-like growth factor II cDNAs from adult bovine and fetal sheep liver.";
RL	Nucleic Acids Res. 18:4614-4614(1990).
RN	[3]
RP	SEQUENCE FROM N.A.
RA	TISSUE=Coopworth; TISSUE=Liver;
RT	MEDLINE=93250051; PubMed=8485157;
RA	Denner J., Hill D.F., Petersen G.B.;
RT	"Characterization of two sheep insulin-like growth factor II cDNAs with different 5'-untranslated regions.";
RL	Biotech. Biophys. Acta 1173:79-80(1993).
RN	[4]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Liver;
RA	Olsen S.M., Wong E.A.;
RL	Submitted (SEP-1990) to the EMBL/GenBank/DDBJ databases.
RN	[5]
RP	SEQUENCE OF 25-91.
RX	MEDLINE=89136887; PubMed=2537174;
RA	Francis G.L., McNeil K.A., Wallace J.C., Ballard F.J., Owens P.C.;
RT	"Sheep insulin-like growth factors I and II: sequences, activities and assays.,"
RL	Endocrinology 124:1173-1183(1989).
RN	[6]
RP	SEQUENCE OF 25-58.
RX	MEDLINE=89123215; PubMed=2752053;
RA	Hey A.W., Browne C.A., Simpson R.J., Thorburn G.D.;
RL	"Simultaneous isolation of insulin-like growth factors I and II from adult sheep serum.";
RL	Biochim. Biophys. Acta 997:27-35(1989).
CC	ACTIVITY: THE INSULIN-LIKE GROWTH FACTORS POSSESS GROWTH-PROMOTING
CC	ACTIVITY: IN VITRO, THEY ARE POWERFUL MITOGENS FOR CULTURED CELLS.
CC	IGF-II IS INFLUENCED BY PLACENTAL LACTOGEN AND MAY PLAY A ROLE IN FETAL DEVELOPMENT.
CC	- - - SUBCELLULAR LOCATION: secreted.
CC	- - - SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
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DR	EMBL; U00668; AAB60626; 1; JOINED.
DR	EMBL; U00566; AAB60626; 1; JOINED.
DR	EMBL; U00567; AAB60626; 1; JOINED.
DR	EMBL; X15248; CA33324; 1; -.
DR	EMBL; X53549; CA33762; 1; -.
DR	EMBL; M89788; AAB31548; 1; -.
DR	EMBL; M89789; AAB31549; 1; -.
DR	EMBL; X55638; CAA9163; 1; -.
DR	PIR; S0858; S04856.
DR	PIR; S08567; S08567.
DR	PIR; S10984; S10984.
DR	PIR; S20731; S20731.
DR	PIR; S32557; S32557.
DR	HSSP; P01344; IGF2.
DR	InterPro; IPR004825; Ins/IGF/relax.
DR	PFam; PF0049; Insulin; 1.
DR	PRINTS; PR00276; INSULINA.
DR	PRINTS; PR00277; INSULINB.
DR	SMART; SM00078; IGF; 1.
DR	PROSITE; PS00262; INSULIN; 1.
KW	Insulin family; Mitogen; Growth factor; Signal.
FT	SIGNAL 1 24
FT	CHAIN 25 91
FT	DOMAIN 25 52
FT	DOMAIN 53 64
FT	DOMAIN 65 85
FT	DOMAIN 86 91
FT	PROPEP 92 179
FT	DISULFID 33 71
FT	DISULFID 45 84
FT	DISULFID 70 75
FT	CONFLICT 46 47
FT	SEQUENCE 179 AA: 19616 MW: 7B369AB572E4378 CRC64;
QY	7 RENVPGHERMGRGRTSREL 26
Db	127 RRGIPAFURARRORTLAKEL 146
RESULT 8	
RC_A_NASP	
ID	RC_A_NASP STANDARD; PRM; 414 AA.
AC	PR8555;
DT	15-JUN-2002 (Rel. 41, Created)
DT	15-JUN-2002 (Rel. 41, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Ribulose bisphosphate carboxylase/oxygenase activase (RUBISCO DE activase) (RA)
GN	RCA OR ALR1533.
OS	Alabaena sp. (strain PCC 7120).
OC	Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX	NBII_TaxID=103690;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=2155285; PubMed=1759840;
RA	Kaneko T., Nakamura Y., Wolk C., Kuritz T., Sasamoto S., Kimura T., Kishida Y., Kohara M., Matsunoto M., Kawashima K., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Tabata S.;
RT	"Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.,"
RL	DNA Res. 8:205-213(2001).
CC	- - - FUNCTION: ACTIVATION OF RUBISCO (RIBULOSE-1,5-BISOPHOSPHATE CARBOXYLASE/OXYGENASE; EC 4.1.1.39) INVOLVES THE ATP-DEPENDENT CARBOXYLATION OF THE EPSILON-AMINO GROUP OF LYSINE LEADING TO A CARBAMATE STRUCTURE (BY SIMILARITY).
CC	- - - SIMILARITY: BELONGS TO THE RUBISCO ACTIVASE FAMILY.
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Query Match	31.4%	Score 44; DB 1; Length 220;	Score 44; DB 1; Length 220;
Best Local Similarity	32.0%	Pred. No. 20;	Pred. No. 20;
Matches	8;	Indels	9;
Conservative	8;	Gaps	0;
QY	1	REBREAKRENPGERMGRGRTSKE	25
DB	108	RLQAMHREKPDYKYPKRRKATAQK	132
RESULT 11			
DOP2,DRONE			
ID DOP2,DRONE		STANDARD:	PRT: 539 AA.
AC Q24563;	Q24569;	Q9VAJ8;	
DT 01-NOV-1997 (Rel. 35, Created)			
DT 01-NOV-1997 (Rel. 35, Last sequence update)			
DT 16-OCT-2001 (Rel. 40, Last annotation update)			
DE Dopamine receptor 2.			
GN DOPR2 OR DOPR9B OR DAMB OR CG18741.			
OS Drosophila melanogaster (fruit fly).			
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;			
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;			
OC Muscomorpha; Ephydriidae; Drosophilidae; Drosophila.			
NCBI_TAXID=727;			
RN [1] - SEQUENCE FROM N.A. (LONG ISOFORM).			
RN STRAIN=canton-S; TISSUE=Head;			
RN MEDLINE=96242088; PubMed=655286;			
RN Feng G., Hannan F., Reale V., Hon Y.Y., Kousky C.T., Evans P.D., Hall L.M.,			
RN Hall L.M.,			
RN "Cloning and functional characterization of a novel dopamine receptor from Drosophila melanogaster,"			
RN J. Neurosci. 16:3925-3933(1996).			
RN [2] - SEQUENCE FROM N.A. (SHORT ISOFORM).			
RN STRAIN=canton-S;			
RN MEDLINE=9628265; PubMed=8663989;			
RN Han K.-A., Millar N.S., Grotewiel M.S., Davis R.L., RT			
RN "DAMB, a novel dopamine receptor expressed specifically in Drosophila mushroom bodies,"			
RN Neuron 16:1127-1135(1996).			
RN [3] - SEQUENCE FROM N.A. (SHORT ISOFORM).			
RN STRAIN=Berkeley;			
RN MEDLINE=20196006; PubMed=10731132;			
RN Adams M.D., Celunker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amarnath S.P.G., Scheerer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Asbury M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H.C., Blazej R.G., Champine M., Prentier B.D., Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbaria A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Balow R.M., Basu A., Baxendale J., Bayartkhangtu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhakraborti D., Bolshakov S., Borikova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burris K.C., Busam D.A., Butler H., Cadle E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Decher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Fosler C., Gabrieli A.E., Garg N.S., Galbraith W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu N.S., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hoskin D., Houston K.A., Howland T.J., Ke M.-H., Ibeagam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., LeI Y., Levitsky R.A., Li J.J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., RA Merrilov G., Milisina N.V., Moharry C., Morris J., Mosirefi A., RA Mount S.M., Moy M., Murphy B., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M., RA Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Sun Y., RA Swarskas R., Tector C., Turner R., Wenter E., Wang A.H., Wang X., RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Robin G.M., Venter J.C.;			
RN "The genome sequence of Drosophila melanogaster."			
RL Science 287:218-2195(2000).			
CC -1 - FUNCTION: RECEPTOR FOR DOPAMINE. THE ACTIVITY OF THIS RECEPTOR IS			
CC -1 - MEDiated BY G PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE. ALSO			
CC CAPABLE OF GENERATING A CALCIUM SIGNAL. IN TERMS OF ANTAGONIST			
CC RESPONSES, WOULD BE CLASSED WITH THE D1-LIKE DOPAMINE RECEPTOR			
CC GROUP. THIS RECEPTOR AN ATTRACTIVE CANDIDATE FOR INITIATING			
CC BIOCHEMICAL CASCADES UNDERLYING OLFACTORY LEARNING.			
CC -1 - SUBCELLULAR LOCATION: Integral membrane protein.			
CC -1 - ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A			
CC SHORT FORM; MAY BE PRODUCED BY ALTERNATIVE SPLICING.			
CC -1 - TISSUE SPECIFICITY: EXPRESSED IN BOTH CENTRAL AND PERIPHERAL			
CC NERVOUS SYSTEMS.			
CC -1 - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
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CC -----			
DR DR PRINTS: PR00237; GPCRDBPSN.			
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL1; 1.			
DR PROSITE: PS00262; G-PROTEIN_RECEP_FL2; 1.			
DR G-protein coupled receptor; Transmembrane; Glycoprotein;			
DR Phosphorylation; Lipoprotein; Palmitate; Alternative splicing.			
DR DOMAIN 1 113 133 1 (POTENTIAL).			
FT TRANSMEM 114 134 1 (POTENTIAL).			
FT DOMAIN 135 145 2 (POTENTIAL).			
FT TRANSMEM 146 166 2 (POTENTIAL).			
FT DOMAIN 167 189 3 (POTENTIAL).			
FT TRANSMEM 190 205 3 (POTENTIAL).			
FT DOMAIN 207 227 3 (POTENTIAL).			
FT TRANSMEM 228 248 4 (POTENTIAL).			
FT DOMAIN 249 266 5 (POTENTIAL).			
FT TRANSMEM 267 287 5 (POTENTIAL).			
FT DOMAIN 288 420 6 (POTENTIAL).			
FT TRANSMEM 421 441 6 (POTENTIAL).			
FT DOMAIN 442 453 7 (POTENTIAL).			
FT TRANSMEM 454 474 7 (POTENTIAL).			
FT DOMAIN 475 539 7 (POTENTIAL).			
FT DOMAIN 86 89 7 (POTENTIAL).			
FT DOMAIN 338 351 7 (POTENTIAL).			
FT DOMAIN 357 367 7 (POTENTIAL).			
FT CARBOHYD 31 31 7 (POTENTIAL).			
FT CARBOHYD 47 47 7 (POTENTIAL).			
FT CARBOHYD 68 68 7 (POTENTIAL).			
FT DISULFID 182 261 7 (POTENTIAL).			
FT LIPID 492 492 7 (POTENTIAL).			
FT LIPID 493 493 7 (POTENTIAL).			
FT VARSPLC 511 539 7 (POTENTIAL).			
FT AASTSCYHHSNQINRHTLM (IN SHORT ISOFORM).			
SQ SEQUENCE 539 AA: 59505 MW: 32FDLDC0E935AF4B3 CRC64;			
Query Match	31.4%	Score 44; DB 1; Length 539;	
Best Local Similarity	34.6%	Pred. No. 52;	
Matches	9;	Indels	0;
Conservative	5;	Gaps	0;
Mismatches	12;		

		Matches	10;	Conservative	4;	Mismatches	6;	Indels	2;	Gaps	1;
Qy	2 LEAKHENYVPGHEFNGRGTSSKELA 27	5	KHRENYPGH- ERMGRGRTSSK 24								
Db	384 LSALHNGLARHHRMGKFLSLRKLA 409	6	;; : :								
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AC 052759;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 16-OCT-2001 (Rel. 40, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE 30S ribosomal protein S4.
 GN RPSD OR PA4239.
 OS *Pseudomonas aeruginosa*.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalek D.J., Lagrou M.,
 RA Garber R.L., Goltry L., Tolentino E., Westbroek-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Labib K., Lin R.M.,
 RA Smith D.H., Wong Z., Paulsen I.T., Reizer J., Sauer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RA "Complete genome sequence of *Pseudomonas aeruginosa* PA01, an
 opportunistic pathogen.";
 RL Nature 406:959-964(2000).
 RN [2]
 RP SEQUENCE OF 189-206 FROM N.A.
 RC STRAIN=FRD1;
 RX MEDLINE=99396583; PubMed=10368148;
 RA Ma J.-F., Ochsner U.A., Klotz M.G., Nanayakkara V.K., Howell M.L.,
 RA Johnson Z., Posey J.E., Vasil M.L., Monaco J.J., Hassett D.J.,
 RT "Bacterioferritin A modulates catalase A (KatA) activity and
 resistance to hydrogen peroxide in *Pseudomonas aeruginosa*.";
 RL J. Bacteriol. 181:3730-3742(1999).
 CC |- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA
 CC |- (BY SIMILARITY).
 CC |- SIMILARITY: CONTAINS 1 S4 RNA-BINDING DOMAIN.
 CC |- SIMILARITY: BELONGS TO THE S4P FAMILY OF RIBOSOMAL PROTEINS.
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 DR EMBL; AE00481; AAG07627.1; -;
 DR EMBL; AF047025; AAC03115.1; -;
 DR HSP; PB1288; IC05.
 DR InterPro; IPR001912; Ribosomal_S4.
 DR InterPro; IPR002942; S4.
 DR Pfam; PF00163; Ribosomal_S4; 1.
 DR Pfam; PRO1479; S4; 1.
 DR SMART; SM00363; S4; 1.
 DR TIGRFAM; TIGR01017; rpsD_bact; 1.
 DR PROSITE; PS00632; RIBOSOMAL_S4; 1.
 KW Ribosomal_protein; rRNA-binding; complete proteome.
 FT 189 194 SDLSRD -> NSSSVP (IN REF. 2).
 SQ SEQUENCE 206 AA; 23277 MN: DBDB5D0191723186 CRC64;
 Query Match 31.1%; Score 43.5; DB 1; Length 206;
 Best local similarity 50.0%; Pred. No. 22;
 Matches 11; Conservative 3; Mismatches 7; Indels 1; Gaps 1;
 QY 2 LEAHR-ENVPGHMRGRTS 22
 QY 1::1 : 1111 1111
 DB 28 LDSCCKAENVPGQHQQRGRRLS 49

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 29, 2002, 13:55:48 ; Search time 79 Seconds

(without alignments) 70.421 Million cell updates/sec

Title: US-09-674-913A-2

Perfect score: 140

Sequence: 1 RLEAKHRENVPGHERMGRGRTSSKELA 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

tal number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%, Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL;21;*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriopl:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	39.3	576	16	Q8X5Z5
2	54.5	38.9	157	16	Q8X5Z5
3	50.5	36.1	251	5	Q8X5Z5
4	50.5	36.1	491	5	Q8X5Z5
5	50.5	35.7	72	16	Q9HTUB
6	50	35.7	838	10	Q9XK9
7	49.5	35.4	424	3	Q74328
8	49.5	35.4	2140	3	Q02316
9	49	35.0	193	5	Q9V712
10	49	35.0	829	16	Q8YQK8
11	48.5	34.6	483	10	Q8SB46
12	48.5	34.6	765	2	Q9K5L1
13	48.5	34.6	765	2	Q9K5K7
14	48	34.3	244	4	Q8Tf63
15	48	34.3	864	4	Q94827
16	34.3				Q96bs1

Result No.	Score	Query Match	Length	DB ID	Description	RESULT 1	PRELIMINARY:	PRT:	576 AA.
1	55	39.3	576	16	Q8X5Z5	Q8X5Z5;	Q8X5Z5;	Q8X5Z5;	Q8X5Z5;
2	54.5	38.9	157	16	Q8X5Z5	01-MAR-2002 (TREMBREL; 20, Created)	01-MAR-2002 (TREMBREL; 20, Last sequence update)	01-MAR-2002 (TREMBREL; 20, Last annotation update)	01-JUN-2002 (TREMBREL; 21, Last annotation update)
3	50.5	36.1	251	5	Q8X5Z5	DE	DE	DE	DE
4	50.5	36.1	491	5	Q8X5Z5	LEU2 OR RSP0322 OR RS05445.			
5	50.5	35.7	72	16	Q9HTUB	OS	OS	OS	OS
6	50	35.7	838	10	Q9XK9	Ralstonia solanacearum (Pseudomonas solanacearum).			
7	49.5	35.4	424	3	Q74328	OG	OG	OG	OG
8	49.5	35.4	2140	3	Q02316	OC	OC	OC	OC
9	49	35.0	193	5	Q9V712	NCBI_TaxID=305;	NCBI_TaxID=305;	NCBI_TaxID=305;	NCBI_TaxID=305;
10	49	35.0	829	16	Q8YQK8	[1]	[1]	[1]	[1]
11	48.5	34.6	483	10	Q8SB46	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
12	48.5	34.6	765	2	Q9K5L1	RA	RA	RA	RA
13	48.5	34.6	765	2	Q9K5K7	RA	RA	RA	RA
14	48	34.3	244	4	Q8Tf63	RA	RA	RA	RA
15	48	34.3	864	4	Q94827	RA	RA	RA	RA
16	34.3				Q96bs1	RA	RA	RA	RA

Result No.	Score	Query Match	Length	DB ID	Description	ALIGNMENTS
1	55	39.3	576	16	Q8X5Z5	Q9JYD2 neisseria m
2	54.5	38.9	157	16	Q8X5Z5	Q9JYD2 neisseria m
3	50.5	36.1	251	5	Q8X5Z5	Q9na31 leishmania
4	50.5	36.1	491	5	Q8X5Z5	Q9m3r3 pinus sylve
5	50.5	35.7	72	16	Q9HTUB	Q9p4t5 cephalospor
6	50	35.7	838	10	Q9XK9	Q9ls5 capricorni
7	49.5	35.4	424	3	Q74328	Q76269 leishmania
8	49.5	35.4	2140	3	Q02316	Q76343 leishmania
9	49	35.0	193	5	Q9V712	Q54170 streptomyce
10	49	35.0	829	16	Q8YQK8	Q8t1p6 mus musculus
11	48.5	34.6	483	10	Q8SB46	Q9ic68 bacillus su
12	48.5	34.6	765	2	Q9K5L1	P79187 macropus gi
13	48.5	34.6	765	2	Q9K5K7	P79198 macropus ru
14	48	34.3	244	4	Q8Tf63	P79417 petrogale b
15	48	34.3	864	4	Q94827	P79418 petrogale b
16	34.3				Q96bs1	P79409 petrogale x
17	48	34.3	576	16	Q9JYD2	P79414 petrogale m
18	48	34.3	576	16	Q9JYD2	P79415 petrogale c
19	48	34.3	576	16	Q9JYD2	P79416 petrogale s
20	47.5	33.9	222	10	Q9M3r3	P79416 petrogale g
21	47.5	33.9	332	3	Q9P4t5	Q9ycml brucella me
22	47.5	33.9	113	6	Q9N5s5	Q97d15 clostridium
23	47	33.6	491	5	Q9JYD2	Q97d15 clostridium
24	47	33.6	491	5	Q9JYD2	Q97d15 clostridium
25	46.5	33.2	382	16	Q9P4t5	Q97d15 clostridium
26	46.5	33.2	476	11	Q8RIP6	Q97d15 clostridium
27	46.5	33.2	770	2	Q9LC68	Q97d15 clostridium
28	46	32.9	87	6	P79187	Q97d15 clostridium
29	46	32.9	87	6	P79198	Q97d15 clostridium
30	46	32.9	188	6	P79417	Q97d15 clostridium
31	46	32.9	188	6	P79418	Q97d15 clostridium
32	46	32.9	188	6	P79409	Q97d15 clostridium
33	46	32.9	188	6	P79414	Q97d15 clostridium
34	46	32.9	188	6	P79415	Q97d15 clostridium
35	46	32.9	188	6	P79416	Q97d15 clostridium
36	46	32.9	188	6	P79417	Q97d15 clostridium
37	46	32.9	188	6	P79418	Q97d15 clostridium
38	46	32.9	188	6	P79419	Q97d15 clostridium
39	46	32.9	188	6	P79411	Q97d15 clostridium
40	46	32.9	188	6	P79412	Q97d15 clostridium
41	46	32.9	188	6	P79408	Q97d15 clostridium
42	46	32.9	188	6	P79416	Q97d15 clostridium
43	46	32.9	302	16	P79416	Q97d15 clostridium
44	46	32.9	313	5	Q9ycml	Q97d15 clostridium
45	46	32.9	342	16	Q97d15	Q97d15 clostridium

QY	1	RLEAKHRENPVGHERRGRGRTSSKELA	27	SEQUENCE	251 AA;	28930 MW;	07CCF55D49E079F9	CRC64;
QY	1	RLEAKHRENPVGHERRGRGRTSSKELA	27	Query Match	36.1%	Score 50.5;	DB 5;	Length 251;
		Best Local Similarity	48.0%	Pred. No. 9;				
		Matches	12;	Conservative	3;	Mismatches	3;	Indels 7; Gaps 1;
QY	10	VPGHERRGRGRTSS-----KELA	27	SEQUENCE	251 AA;	28930 MW;	07CCF55D49E079F9	CRC64;
Db	153	LPSPHERGLGLRSLSOFTIELTLEKELA	177	Query Match	36.1%	Score 50.5;	DB 5;	Length 251;
Db	09HT08	PRELIMINARY;	PRT;	157 AA.	Best Local Similarity	48.0%	Pred. No. 9;	Length 251;
ID	09HT08;				Matches	12;	Conservative	3;
ID	09HT08;				Mismatches	3;	Indels 7; Gaps 1;	
DT	01-MAR-2001 (TREMBLrel. 16, Created)							
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)							
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)							
DE	Hypothetical protein PA5246.							
GN	PA5246.							
OS	Pseudomonas aeruginosa.							
OC	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;							
OC	Pseudomonas;							
NCBI_TAXID=287;								
[1]	SEQUENCE FROM N.A.							
STRAIN=ATCC 15692 / PA01;								
MEDLINE=20137337; PubMed=10984043;								
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,								
Hickey M.J., Brinkman F.S.L., Ruffnagle W.O., Kowalk D.J., Legrou M.,								
Garber R.L., Gostry L., Molentino E., Westbrock-Wadman S., Yuan Y.,								
Brody L.R., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,								
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,								
Reizer J., Sauer M.H., Hancock R.E.W., Lory S., Olson M.V.;								
"Complete genome sequence of Pseudomonas aeruginosa PA01, an								
opportunistic pathogen.;"								
RL	Nature 408:959-964(2000); -.							
DR	EMBL; AE004937; AAG08631; -.							
DR	InterPro; IPR00736; DUF157.							
DR	PFAM; PF02384; DUF157; 1.							
DR	PIR; TIGR00369; unchar dom 1; 1.							
KW	Hypothetical protein; Complete proteome; Sequence 157 AA; 17005 MW; 1002F16B858253A3 CRC64;							
SQ	Query Match	38.9%	Score 54.5;	DB 16;	Length 157;			
	Best Local Similarity	40.0%	Pred. No. 1.3;					
	Matches	14;	Conservative	2;	Mismatches	0;	Indels 19;	Gaps 2;
QY	5	KHRENPGHERM-----GRGRT 21						
Db	85	RHRE-LPGHERMARLKGITDLRVYDLRPGRGRT 118						
SQ	GULT 3							
09SF6	PRELIMINARY;	PRT;	251 AA.					
09SF6;								
09SF6;								
01-DEC-2001 (TREMBLrel. 19, Created)								
01-DEC-2001 (TREMBLrel. 19, Last sequence update)								
01-MAR-2002 (TREMBLrel. 20, Last annotation update)								
DE	GH2883P.							
OS	Drosophila melanogaster (Fruit fly).							
OC	Bukarvota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;							
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;							
OC	Ephydioidea; Drosophilidae; Drosophila.							
OX	NCBI_TaxID=7227;							
RN	SEQUENCE FROM N.A.							
RC	STRATM=BERKELEY;							
RA	Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,							
RA	Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,							
RA	Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,							
RA	Nuno J., Paclek J., Paragas V., Park S., Phouanavong S., Wan K.,							
RA	Yu C., Lewis S.E., Rubin G.M., Celinker S.,							
RL	Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.							
DR	EMBL; AY060818; AY123661.1. .							
DR	FlyBase; FlyBase; Fgn003474; CG2640.							
DR	FlyBase; FBgn003474; CG2640.							
DR	EMBL; AY060818; AY123661.1. .							
DR	FlyBase; Fgn003474; CG2640.							
DR	EMBL; AY060818; AY123661.1. .							
DR	FlyBase; FBgn003474; CG2640.							
DR	EMBL; AY060818; AY123661.1. .							
DR	FlyBase; Fgn003474; CG2640.							
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DR	FlyBase; FBgn003474; CG2640.							
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DR	FlyBase; Fgn003474; CG2640.							
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DR	FlyBase; FBgn003474; CG2640.							
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DR	FlyBase; Fgn003474; CG2640.							
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DR	FlyBase; FBgn003474; CG2640.							
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DR	FlyBase; Fgn003474; CG2640.							
DR	EMBL; AY060818; AY123661.1. .							
DR	FlyBase; FBgn003474; CG2640.							
DR	EMBL; AY060818; AY123661.1. .							
DR	FlyBase; Fgn003474; CG2640.							
DR	EMBL; AY060818; AY123661.1. .							
DR	FlyBase; FBgn003474; CG2640.							
DR	EMBL; AY060818; AY123661.1. .							
DR	FlyBase; Fgn003474; CG2640.							
DR	EMBL; AY060818; AY123661.1. .							
DR	FlyBase; FBgn003474; CG2640.							
DR	EMBL; AY060818; AY123661.1. .							
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DR	FlyBase; FBgn003474; CG2640.							
DR	EMBL; AY060818; AY123661.1. .							
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DR	EMBL; AY060818; AY123661.1. .							
DR	FlyBase; FBgn003474; CG2640.							
DR	EMBL; AY060818; AY123661.1. .							
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DR	FlyBase; Fgn003474; CG2640.							
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DR	FlyBase; FBgn003474; CG2640.							
DR	EMBL; AY060818; AY123661.1. .							
DR	FlyBase; Fgn003474; CG2640.							
DR	EMBL; AY060818; AY123661.1. .							
DR	FlyBase; FBgn003474; CG2640.							
DR	EMBL; AY060818; AY123661.1. .							
DR	FlyBase; Fgn003474; CG2640.							
DR	EMBL; AY060818; AY123661.1. .							
DR	FlyBase; FBgn003474; CG2640.							
DR	EMBL; AY060818; AY123661.1. .							
DR	FlyBase; Fgn003474; CG2640.							
DR	EMBL; AY060818; AY123661.1. .							
DR	FlyBase; FBgn003474; CG2640.							
DR	EMBL; AY060818; AY123661.1. .							
DR	FlyBase; Fgn003474; CG2640.							
DR	EMBL; AY060818; AY123661.1. .							
DR	FlyBase; FBgn003474; CG2640.							
DR	EMBL; AY060818; AY123661.1. .							
DR	FlyBase; Fgn003474; CG2640.							
DR	EMBL; AY060818; AY123661.1. .							
DR	Fly							

Matches	12;	Conservative	3;	Mismatches	3;	Indels	7;	Gaps	1;	RESULT 5	7
QY	10	VGHERMGRGRTSS-----KELA	27							09CIP3	PRELIMINARY;
Db	171	LPSHERLGLGRSISQSFYELTKELA	195							09CIP3	PRT;
										09CIP3	72 AA.
										01-JUN-2001	(TREMBrel. 17, Last sequence update)
										01-MAR-2002	(TREMBrel. 20, Last annotation update)
										DE	Hypothetical protein ydbc
										GN	YDBC OR LL0313.
										OS	Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
										OC	Bacteria; Firmicutes; Bacilli; Clostridia group; Lactobacillales;
										OC	Streptococcaceae; Lactococcus.
										NCBI_TAXID	1360;
										NCBI_TAXID	[1]
										SEQUENCE FROM N.A.	
										STRAIN	=ILL403;
										RX	RETRIEVE
										RA	Boilotin A., Wincker P., Mauzer S., Jallion O., Malarrie K.,
										RA	Weissenbach J., Ehrlich S.D., Sorokin A.;
										RT	"The complete genome sequence of the lactic acid bacterium Lactococcus
										RL	lactis ssp. lactis IL1403."
										RL	Genome Res. 11:731-753 (2001).
										DR	EMBL; AL006208; AAC04411.1; -.
										KW	Hypothetical protein; Complete proteome.
										SEQUENCE	72 AA; 8405 MW; C5041FC4543B8410 CRC64;
QY	11	PGHERMGRGRTSSKE	25							QY	11 PGHERMGRGRTSSKE 25
										QY	35.7%; Score 50; DB 16; Length 72;
										Db	Best Local Similarity 60.0%; Pred. No. 2.8; Matches 9; Conservative 9; Mismatches 3; Indels 3; Gaps 0; Gaps 0;
QY	46	PDHEKMGKGITLSE	60							QY	46 PDHEKMGKGITLSE 60
										QY	35.7%; Score 50; DB 16; Length 72;
										Db	Best Local Similarity 60.0%; Pred. No. 2.8; Matches 9; Conservative 9; Mismatches 3; Indels 3; Gaps 0; Gaps 0;
RESULT 6										QY	4 AKHRENVPGHERMGRGRTSSKELA 27
Q9XIX9										Db	SEQUENCE 424 AA; 46955 MW; 4F1B69E61413F9A3 CRC64;
ID	Q9XIX9									QY	4 AKHRENVPGHERMGRGRTSSKELA 27
AC	Q9XIX9;									Db	169 AKEKSLIP--RRSRGRTSSKLS 189
DT	01-NOV-1999	(TREMBrel. 12, Created)								QY	4 AKHRENVPGHERMGRGRTSSKELA 27
DT	01-NOV-1999	(TREMBrel. 12, Last sequence update)								Db	169 AKEKSLIP--RRSRGRTSSKLS 189
DT	01-NOV-1999	(TREMBrel. 12, Last annotation update)								QY	4 AKHRENVPGHERMGRGRTSSKELA 27
DT	01-NOV-1999	(TREMBrel. 12, Last annotation update)								Db	169 AKEKSLIP--RRSRGRTSSKLS 189
DT	01-NOV-1999	(TREMBrel. 12, Last annotation update)								QY	4 AKHRENVPGHERMGRGRTSSKELA 27
OS	Oryza sativa	(Rice).								Db	169 AKEKSLIP--RRSRGRTSSKLS 189
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;									QY	4 AKHRENVPGHERMGRGRTSSKELA 27
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;									Db	169 AKEKSLIP--RRSRGRTSSKLS 189
OX	Embrionidae; Oryzeae; Oryza.									QY	4 AKHRENVPGHERMGRGRTSSKELA 27
NCBI_TAXID	=4530;									Db	169 AKEKSLIP--RRSRGRTSSKLS 189
RN	[1]									QY	4 AKHRENVPGHERMGRGRTSSKELA 27
SEQUENCE FROM N.A.										Db	169 AKEKSLIP--RRSRGRTSSKLS 189
RC	STRAIN=CV_NIPPONNARE;									QY	4 AKHRENVPGHERMGRGRTSSKELA 27
RA	"Oryza sativa nipponbare(G13) genomic DNA, chromosome 6, PAC									Db	169 AKEKSLIP--RRSRGRTSSKLS 189
RT	clone:PG681F10.;"									QY	4 AKHRENVPGHERMGRGRTSSKELA 27
RL	Submitted (ARR-1999) to the EMBL/GenBank/DBJ databases.									Db	169 AKEKSLIP--RRSRGRTSSKLS 189
DR	EMBL; AB026295; BRA81852.1; -.									QY	4 AKHRENVPGHERMGRGRTSSKELA 27
SEQUENCE	838 AA;	92789 MW;								Db	169 AKEKSLIP--RRSRGRTSSKLS 189
Query Match	35.7%; Score 50; DB 10; Length 838;									QY	4 AKHRENVPGHERMGRGRTSSKELA 27
Best Local Similarity 48.0%; Pred. No. 40; Matches 12; Conservative 12; Mismatches 12; Indels 0; Gaps 0;										Db	169 AKEKSLIP--RRSRGRTSSKLS 189
RESULT 7										QY	4 AKHRENVPGHERMGRGRTSSKELA 27
ID	074328									Db	169 AKEKSLIP--RRSRGRTSSKLS 189
AC	074328; Q9USG2;									QY	4 AKHRENVPGHERMGRGRTSSKELA 27
DT	01-NOV-1998 (TREMBrel. 08, Created)									Db	169 AKEKSLIP--RRSRGRTSSKLS 189
DT	01-MAR-2002 (TREMBrel. 20, Last annotation update)									QY	4 AKHRENVPGHERMGRGRTSSKELA 27
DE	Hypothetical 47.0 kDa protein C1685.08 in chromosome 1R.									Db	169 AKEKSLIP--RRSRGRTSSKLS 189
GN	SPBC1685.08.									QY	4 AKHRENVPGHERMGRGRTSSKELA 27
OS	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetaceae;									Db	169 AKEKSLIP--RRSRGRTSSKLS 189
OC	Schizosaccharomyces pombe (Fission Yeast).									QY	4 AKHRENVPGHERMGRGRTSSKELA 27
OC	Schizosaccharomyces pombe (Fission Yeast).									Db	169 AKEKSLIP--RRSRGRTSSKLS 189
RN	[1]									QY	4 AKHRENVPGHERMGRGRTSSKELA 27
RP	SEQUENCE FROM N.A.									Db	169 AKEKSLIP--RRSRGRTSSKLS 189
RC	STRAIN=972;									QY	4 AKHRENVPGHERMGRGRTSSKELA 27
RA	Wood V., Rejandream M.A., Barrell B.G., Hilbert H., Duesterhoeft A.									Db	169 AKEKSLIP--RRSRGRTSSKLS 189
RL	Submitted (JUL-1998) to the EMBL/GenBank/DDJB databases.									QY	4 AKHRENVPGHERMGRGRTSSKELA 27
RP	SEQUENCE OF 114-179 FROM N.A.									Db	169 AKEKSLIP--RRSRGRTSSKLS 189
RC	STRAIN=968 H90;									QY	4 AKHRENVPGHERMGRGRTSSKELA 27
RA	Ding D.,									Db	169 AKEKSLIP--RRSRGRTSSKLS 189
RT	"Generation and analysis of GFP-gene fusion library of fission yeast."									QY	4 AKHRENVPGHERMGRGRTSSKELA 27
RL	Submitted (MAY-1999) to the EMBL/GenBank/DDJB databases.									Db	169 AKEKSLIP--RRSRGRTSSKLS 189
CC	[1] - SIMILARITY: TO YEAST YPL181W.									QY	4 AKHRENVPGHERMGRGRTSSKELA 27
DR	EMBL; AL031154; CAA20056.1; -.									Db	169 AKEKSLIP--RRSRGRTSSKLS 189
DR	EMBL; AB027769; BAA87073.1; -.									QY	4 AKHRENVPGHERMGRGRTSSKELA 27
DR	InterPro; IPR019655; Znf-PHD.									Db	169 AKEKSLIP--RRSRGRTSSKLS 189
PRAM	SMART; PF00628; PHD; 1.									QY	4 AKHRENVPGHERMGRGRTSSKELA 27
DR	SMART; SM00249; PHD; 1.									Db	169 AKEKSLIP--RRSRGRTSSKLS 189
KW	Hypothetical protein.									QY	4 AKHRENVPGHERMGRGRTSSKELA 27
SQ	SEQUENCE									Db	169 AKEKSLIP--RRSRGRTSSKLS 189
RESULT 8										QY	4 AKHRENVPGHERMGRGRTSSKELA 27
Q02316										Db	169 AKEKSLIP--RRSRGRTSSKLS 189
ID	Q02316									QY	4 AKHRENVPGHERMGRGRTSSKELA 27
AC	002316;									Db	169 AKEKSLIP--RRSRGRTSSKLS 189
DT	01-NOV-1996 (TREMBrel. 01, Created)									QY	4 AKHRENVPGHERMGRGRTSSKELA 27
DT	01-JAN-1999 (TREMBrel. 09, Last sequence update)									Db	169 AKEKSLIP--RRSRGRTSSKLS 189
DT	01-MAR-2002 (TREMBrel. 20, Last annotation update)									QY	4 AKHRENVPGHERMGRGRTSSKELA 27
DE	Mature fruiting body-specific cell-adhesion protein (MFBA).									Db	169 AKEKSLIP--RRSRGRTSSKLS 189
MFBA	OR MFBI.									QY	4 AKHRENVPGHERMGRGRTSSKELA 27
OS	Lentinula edodes (Shiitake mushroom) (Lentinus edodes).									Db	169 AKEKSLIP--RRSRGRTSSKLS 189
OC	Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Agaricales; Tricholomataceae; Lentinula.									QY	4 AKHRENVPGHERMGRGRTSSKELA 27
OK	NCBI_TAXID=5353;									Db	169 AKEKSLIP--RRSRGRTSSKLS 189
RN	[1]									QY	4 AKHRENVPGHERMGRGRTSSKELA 27
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 565-570.									Db	169 AKEKSLIP--RRSRGRTSSKLS 189
RC	STRAIN=FM22;									QY	4 AKHRENVPGHERMGRGRTSSKELA 27
RX	MEDLINE=9512308; PubMed=7867945;									Db	169 AKEKSLIP--RRSRGRTSSKLS 189
RA	Kondo O., Moto A., Kajiwara S., Takagi J., Saito Y., Shishido K.;									QY	4 AKHRENVPGHERMGRGRTSSKELA 27
RT	"A fruiting body-specific cDNA, mfbac, from the mushroom Lentinus edodes encodes a high-molecular-weight cell-adhesion protein containing an Arg-Gly-Asp motif."									Db	169 AKEKSLIP--RRSRGRTSSKLS 189
RT	Gene 154:31-37 (1995).									QY	4 AKHRENVPGHERMGRGRTSSKELA 27
RL	-i- FUNCTION: MAY PLAY A ROLE IN CELL ADHESION.									Db	169 AKEKSLIP--RRSRGRTSSKLS 189
CC	-i- TISSUE SPECIFICITY: FRUITING BODY-SPECIFIC. HIGHLY EXPRESSED IN THE PILEUS; MODERATE EXPRESSION IN THE STIPE; LOW LEVELS OF EXPRESSION IN THE GILLS.									QY	4 AKHRENVPGHERMGRGRTSSKELA 27
CC	-i- DEVELOPMENTAL STAGE: EXPRESSION IS HIGH IN MATURE FRUITING BODIES BUT ABSENT IN EARLIER									Db	169 AKEKSLIP--RRSRGRTSSKLS 189
CC	DETECTABLE IN IMMATURE FRUITING BODIES.									QY	4 AKHRENVPGHERMGRGRTSSKELA 27

CC	-I- SIMILITRY CONTAINS 1 SET DOMAIN.
DR	SPAGES OF DEVELOPMENT AND IN THE VEGETATIVE MYCELLUM.
EMBL; DR4487; BAA18903.1; -.	RA Wang Y.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Svirkas R., Tector C., Turner R., Venter J.C., Wang A.H., Wang X., Williams S.M., Woodage T., Wolley K.C., Wu D., Yang S., Yao Q.A., Williams S.M., Woodage T., Wolley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhang M., Zhang G., Zhao Q., Zheng L., InterPro; IPR01214; SET.
DR	InterPro; IPR01965; Znf PHD.
DR	Pfam; PF00628; PHD; 1.
DR	Pfam; PF00356; SET; 1.
DR	SMART; SM00249; PHD; 1.
DR	SMART; SM0317; SET; 1.
DR	PROSITE; P50280; SET; 1.
FT	cell adhesion.
FT	DOMAIN 144 195 CYS-RICH (PHD-FINGER).
FT	DOMAIN 376 548 SET DOMAIN. CELL ATTACHMENT SITE (POTENTIAL).
FT	DOMAIN 795 797 SITE (POTENTIAL).
FT	SEQUENCE 2140 AA; 232670 MW; 95CB36DE3A77CBFB CRC64;
Query Match	35.4%; Score 49.5; DB 3; Length 2140;
Best Local Similarity	33.3%; Pred. No. 1, 3e+02;
Matches	12; Conservative 6; Mismatches 7; Indels 11; Gaps 1;
Db	159 EAKDKENLPDHWCWECDPSSLERIDREKARSLOIA 194
RESULT 9	
09V712	PRELIMINARY; PRT; 193 AA.
ID	09V712; 09V712; 01-MAY-2000 (TREMBLrel. 13, Created)
AC	09V712; 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE	CG13941 protein.
DE	Drosophila melanogaster (Fruit fly).
GN	CG13941.
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Anthropoda; Tracheata; Hexapoda; Insecta; Muscomorpha;
OC	Phrygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Diptera; Dirosophilidae; Drosophila.
RP	NCBI_TaxID=7227;
RX	SEQUENCE FROM N.A.
RX	MEDLINE=20196006; Pubmed=10731132;
RA	Adams M.D., Celinkin S.E., Holt R.R., Evans C.A., Gocayne J.D., Amanatides P.G., Scheer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazquez R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., April J.F., Agbavai A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Balleil R.M., Basu A., Baxendale H., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burt D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Dietz S.M., Mays A.D., New I., Dunn P., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin R.K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Fosler C., Gabrilian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Inegwam C., Jalali M., Kaliush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei P., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moskrefi A., Mount S.M., Moy M., Murphy B., Murphy D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RESULT 10	
08Y048	PRELIMINARY; PRT; 829 AA.
ID	08Y048; 08Y048; 01-MAR-2002 (TREMBLrel. 20, Created)
AC	08Y048; 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE	Hypothetical protein Alr3815.
GN	GN ALR3815.
OS	Anabaena sp. (strain PCC 7120).
OC	Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX	NCBI_TaxID=103690; [1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=21395285; Pubmed=11759840;
RA	Kaneiro T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriyuchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsuno M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.
RA	Yasuda M., Tabata S.;
RA	Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.;
RA	DNA Res. 8; 205-213(2001).
RA	EMBL; AP003594; BAB75514.1; -.
DR	InterPro; IPR002048; EF-hand.
DR	InterPro; IPR013100; protease_C2.
DR	Pfam; PF00648; Peptidase_C2; 1.
DR	SMART; SM00230; CYPRC; 1.
DR	PROSITE; PS00018; EF_HAND; UNKNOWN_1.
KW	Hypothetical protein; Complete proteome.
SEQUENCE	829 AA; 89203 MW; 8B2D05E2731AF33 CRC64;
Query Match	35.0%; Score 49; DB 16; Length 829;
Best Local Similarity	45.0%; Pred. No. 56;
Matches	9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
Db	704 RENTPGYLNIGDNLNRL 723
RESULT 11	
08SB46	PRELIMINARY; PRT; 483 AA.
ID	08SB46; 08SB46; 01-JUN-2002 (TREMBLrel. 21, Created)
AC	08SB46; 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE	Putative polyprotein.
GN	OSJNBB0931009.13.

OS	Oryza sativa (Rice).
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC	Bacillaceae; Bacillus.
OC	NCBI_TaxID=72360;
RN	[1] SEQUENCE FROM N.A.
RP	RA Torroso P., Logsdon L., Kraigher B., Itoh Y., Mandic-Mulec I.,
RA	DR Dubnau D.;
RA	RT "Specificity and genetic polymorphism of the Bacillus competence quorum-sensing system.", to the EMBL/GenBank/DBJ databases.
RA	RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RT	DR EMBL; AC01732; AAL717162; 1; -.
RL	DR POLYPROTEIN.
DR	DR EMBL; AC01732; AAL717162; 1; -.
KW	SEQUENCE
QY	4 AKHRENVPGHEMRGGRGRTSSKEL 26
DB	107 AKHNMVAPVHQTSRAETNSNKOI 130
RESULT 12	
09K5L1	Query Match
ID	Best Local Similarity 34.6%; Score 48.5; DB 10; Length 483;
09K5L1	Matches 11; Conservative 4; Mismatches 8; Indels 1; Gaps 1;
PRELIMINARY; PRT; 765 AA.	
AC	AC 01-OCT-2000 (TREMBLrel. 15, Created)
DT	DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT	DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE	DE Comp.
OS	OS Bacillus subtilis.
OC	OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC	RC STRAIN=RS-B-1;
OX	OX NCBI_TaxID=1423;
RP	RP SEQUENCE FROM N.A.
RA	RA Tortosa P., Logsdon L., Kraigher B., Itoh Y., Mandic-Mulec I.,
RA	DR Dubnau D.;
RA	RT "Specificity and genetic polymorphism of the Bacillus competence quorum-sensing system.", to the EMBL/GenBank/DBJ databases.
RA	RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR	DR EMBL; AY00390; ARF8174; 1; -.
DR	DR InterPro; IPR03594; ATPbind_Atpase.
DR	DR InterPro; IPR03661; His_KinA.
DR	DR InterPro; IPR04359; HIS_KIN_sig.
DR	DR PROSITE; PS50106; PDZ; 1.
DR	DR PROSITE; PS50106; PDZ; 1.
DR	DR SEQUENCE; 765 AA; 8805 MW; 725552C6A8B76A62 CRC64;
RESULT 13	
09K5K7	Query Match
ID	Best Local Similarity 34.6%; Score 48.5; DB 2; Length 765;
09K5K7	Matches 12; Conservative 6; Mismatches 8; Indels 1; Gaps 1;
PRELIMINARY; PRT; 765 AA.	
AC	AC 01-OCT-2000 (TREMBLrel. 15, Created)
DT	DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT	DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE	DE Comp.
OS	OS Bacillus mojavensis.
RESULT 14	
08TF63	Query Match
ID	Best Local Similarity 34.6%; Score 48.5; DB 2; Length 765;
08TF63	Matches 12; Conservative 4; Mismatches 6; Indels 1; Gaps 1;
PRELIMINARY; PRT; 244 AA.	
AC	AC 08TF63; 1
DT	DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT	DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
Db	Db 645 KIVAOQQQSERPVPHIRNQRTFRLSDL 671
GN	GN DCNP1.
OS	OS Homo sapiens (Human).
OC	OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	OC Mammalia; Eutheria; Primates; Cattarrhini; Hominoidea; Homo.
OX	OX NCBI_TaxID=9606;
RN	[1] SEQUENCE FROM N.A.
RP	RP MEDLINE=21656978; PubMed=11798177;
RP	RP Matsuda M., Senjo S., Fujii S., Terasaki Y., Takeya M., Hashimoto S.,
RA	RA Matsushima K., Yumoto E., Nishimura Y.;
RT	RT "Identification and Immunocytochemical Analysis of DCNP1, a Dendritic Cell-Associated Nuclear Protein,"
RT	RT Biochem. Biophys. Res. Commun. 290:1022-1029 (2002).
DR	DR EMBL; AB074498; BAB84585; 1; -.
SQ	SQ SEQUENCE 244 AA; 25704 MW; 803125CEFA61B9F8 CRC54;
QY	8 ENVPHERMRG 19
DB	645 KIVAQQQSERPVPHIRNQRTFRLSDL 671
RESULT 15	
09K5K7	Query Match
ID	Best Local Similarity 34.3%; Score 48; DB 4; Length 244;
09K5K7	Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
PRELIMINARY; PRT; 864 AA.	
AC	AC 094827; 1
DT	DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT	DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT	DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE	DE KIAA0720 Protein (Fragment).

GN_KIAA0720.
 OS_Homo sapiens (Human).
 OC_Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi;
 OC_Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX_NCBI_TaxID=9606;
 RN_11
 RP_SEQUENCE FROM N.A.
 RC_TISSUE=BRAIN;
 RX_MEDLINE=99087487; PubMed=9872452;
 RA_Negase T., Ishikawa K., Suyama M., Kikuno R., Miyajima N., Tanaka A.,
 RA_Kotani H., Nomura N., Ohara O.;
 RT_The complete sequences of 100 new cDNA clones from brain which code
 for large proteins in vitro.;
 RT_DNA Res. 5:277-286(1998).
 RL_EML1; AB018263; BAA3440.1; -.
 DR_InterPro; IPR01849; PH.
 DR_InterPro; IPR00219; RhoGEF.
 DR_Pfam; PF00169; PH; 1.
 DR_Pfam; PRO0621; RhoGEF; 1.
 DR_SMART; SW00233; PH; 1.
 DR_SMART; SW00325; RhoGEF; 1.
 DR_Prosite; PS50003; PH_DOMAIN; 1.
 FT_NON_TER_1
 SQ_1
 SEQUENCE 864 AA; 95282 MW; 1EA2E7DB43E595D7 CRC64;
 Query Match 34.3%; Score 48;
 Best Local Similarity 40.0%; Pred. No. 84; Length 864;
 Matches 10; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
 QY 1 RLEAKHRENVPGHERRMGRGRTESSKE 25
 QY 1 ||| || : ||| : | : |
 Db 173 RLEDSWRELDGHEKLTRRQHOOE 197

Search completed: October 29, 2002, 13:57:35
 Job time : 80 secs